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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 (bases 1 to 983)
Hansen, P. Kamp., Wagner, P., Mullertz, A. Animal feed additives
Patent: US 6245546-A 1 12-JUN-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGGTGGAGCCCAGCCTACACCCAACCTGGAAGGCGCACCTACGAGATCAGCTGG
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                                                                                                                                                       GAGCCTGGCCAGGATCAGTAGTTGCTTTGCGGTGTTTTTGCTCCCTATTCTCGTGAAAAAA
                                                                                                                                                                                                                                                         TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA
                                                                                                                                                                                                                                                                                          TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACCTGG
                                                                                                                                                                                                                                                                                                           TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACCTGG
                                                                                                                                                                                                                                                                                                                                          GCTCGCCCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGC
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                                                                                                      TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA
                                                                                                                                         GAGCCTGGCCAGGATCAGTAGTTGCTTTGCGGTGTTTTGCTCCCTATTCTCGTGAAAAAA
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                                                                                                                                                                                                      ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC
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Biocatalysis, TU-Graz, Petersgasse 12,, Graz 8010, Austria
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2460 bp DNA linear PLN 15-NOV-20
Thermomyces lanuginosus endo-beta-1,4-D-xylanase precursor (xynA)
gene, complete cds.
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Bukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.

1 (bases 1 to 2460)

Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H.

Schlacher, B., Holzmann, C., Hayn, M., Steiner, W. and Schwab, H.

Cloning and characterization of the gene for the thermostable xylanase XynA from Thermomyces lanuginosus

J. Blotechnol. 49 (1-3), 211-218 (1996)
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  CGACAGACACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGT 180
                                       GCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCTCGAAAAG 1154
                                                            GCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGGAATGCCCACGGAGCTCGAAAAG 120
                                                                                                                      TCGGCCCGACGTCTTGCAATCCTTGCAGTGATGGTCGGCTTTACCCCCGTTGCCCTTGCG
                                                                                                                                            TCGGCCCGACGTCTTGCAATCCTTGCAGTGATGGTCGGCCTTTACCCCCCGTTGCCCCTTGCG 60
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                                                                                                                                                                                                  Conservative
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SYLAVYGWTRNPLVEYYIVENFGTYQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYAR
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860. .863
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860. .2106
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/gene="xynA"
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join(1030. .1330,1437. .2106)
/gene="xynA"
                                                                                                                                                                                                                                                                                                                                       /product="endo-beta-1,4-D-xylanase"
/note="determined by homology"
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join(1158. .1330,1437. .1845)
/gene="xynA"
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join(1065. .1330,1437. .1848)
gene="xynA"
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/strain="DSM 5826"
                                                                                                                                                                                                                                                                                                'gene≖"xynA"
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SOURCE
    ORGANISM
Thermomyces lanuginosus Thermomyces lanuginosus
                                                                            588 bp Sequence 9 from Patent WO0166711.
                                                            AX244978.1
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GCTTTCCTCACCCCAACCGCAACAGCTAGCTAACCTGTCCACTTTGAGGG
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DNA

linear

PAT 28-SEP-2001

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Schulte, U., Holland, R., Unpublished
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Xylanase variants having altered sensitivity to Patent: WO 0166711-A 9 13-SEP-2001;

DANISCO A/S (DK)
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BX842624
BX842624.1 GI:38566913
                                                                                                                                   Neurospora
Eukaryota;
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/mol_type="unassigned D
/db_xref="taxon:5541"
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Fungi; Ascomycota; Pezizomycotina;
Fungi; Ascomycota; Sordariaceae;
                                                                                                                                                                                      crassa
                           Aign, V., Hoheisel, J., Nyakatura, G., Mewes, H.
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100.0%; Pred. No. 3.3e-128;
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Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, B-mail:
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, B-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
B-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, http://www.fgsc.net
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation of this entry and other sequences can be viewed http://mips.gsf.de/proj/neurospora.
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German Neurospora genome, project.
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complement (Join (4810. .5445,5507. .5563))

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ARCHWLYAFFEDGGWPKPENDHVWGAPEAPELRLVTPEGDVWWLDDPVDYEALPWEREV
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fdvlhspspkkrltrryfnpgsrppfpattargisfnyrtplknttatktddhladt
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      complement (8441. .9241)
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                                                                'gene="B10D6.050"
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CCCTTCGTCGGGCGCCCAACGTCTCGGATCCGTCTACACCGACGGCTCCACCTACGACAT 38926
                                                                                                                                                                                                                                                                               CAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGC 293
                                      TCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACT
                                                                                                                          CGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGA 413
                                                                                                                                                                 TCGCACCATCACCTACTCGGGTAACTTCAGACCCTCGGGCAACGGCTACCTGTCCGTCTA
                                                                                                                                                                                                        AAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTA 353
                                                                                                                                                                                                                                                   GAACTGGCAGAACGCCGGCAACTTTGTCGCCGGCAAGGGCTGGAACCCCCGGTTCG---
                                                                                                                                                                                                                                                                                                                                  CTGGACCGACAACGGCGCAATGTCAACTACGCCAACGGCGCCCAGCGGCTCTTACTCTGT 39163
                                                                                                                                                                                                                                                                                                                                                                         GTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                CGCCGAGCGTGGCGGTACCCCCAGCAGCACCGGCTTCAACAACGGCTTCTACTACTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCTCGGCGCTGCCGGTGCCCTCGCTATGCCCCTTCAACGCCACCGAGTTCTCTGAGCT 39283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTGCGGCCTTAGCCGCGACTGGGGCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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<u>.</u>

2.1e-51;

216;

Indels

6;

Gaps

2

-GC 39106

233 39223

, 39046

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12129...12141,12579...12829,13172...13577,13679...14071,
14173...14195,14433...14924,14995...15128,15186...15281,
15411...15458))
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                                                                                                                                                                                                             QRGSQFAPAPAPAPAPTLLHTCTETSHRAPIFQPTHSTPPRPTPRLPHCRRYRTDIVA
KPNNDLDMLRALQYHRAMARASEQQEATIEAPIHHPYQQGEAQPFRRATLRDCFPQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene:CG11008, Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="B1DD6.060"
/gene="B1DD6.060"
/note="weak similarity to N-terminal region of
/note=""weak similarity to N-terminal region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKLRHRCTWIPVPEKRPIEQLSGDVSVPGLVLTSAEGGNFSLHDPAEL"
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/gene="B10D6.060"
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codon_start=1
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                                                 26.7%;
Score 262.4; D
Pred. No. 2.1e-
0; Mismatches
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                                                                                                         DB 15;
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.13577,13679. .14071,
.15128,15186. .15281,
                                                                                                   Length 89019;
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RESULT 6
TRU24191
LOCUS
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AUTHORS
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                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                            sig_peptide
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                                406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypocrea jecorina
Hypocrea jecorina
Hypocrea jecorina
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sord
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypo
1 (bases 1 to 786)
1 Grange, D.C., Pretorius, I.S. and van Zyl, W.H.
Expression of a Trichoderma reesei beta-xylanase g
Saccharomyces cerevisiae
Sppl. Environ. Microbiol. 62 (3), 1036-1044 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRU24191 786 bp
Trichoderma reesei beta-xylanase
U24191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-APR-1995) Willem H. van Stellenbosch, Microbiology, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U24191.1 GI:780815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van Zyl,W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACAAGACCACCCGCTACAACCAGCCGTCCATTGACGGCACCCGCACCTTCAACCAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGTCGGTCCGCCAGCAGAAGCGCACCGGTGGTACCGTCACCATGGCCAACCACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGGGATACCAGAGCAGTGGCTCTGCCCAGATCACCGTT 38709
   TCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 786)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Africa
                                                                                                                                                                                                                             /trānslation="MVSFTSLLAGVAAISGVLAAPAAEVEPVAVEKRQTIQPGTGYNN
GYPHSYMNDGHGGYTYINGPGGGPSVNWSNSGNEVGGKGWQPGTGXKVINEKGSSYNDN
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/gene="XYN2"
                                                                                                                        /gene="XYN2"
/product="beta-xylanase"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="XYN2"
|05. .776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Hypocrea jecorina"
|mol_type="mRNA"
|strain="QM 6a"
                                                                                                                                                                                                                                                                                                                                                                        note="endo-beta-1,4-xylanase; endoxylanase"
                                                                                                                                                                                                                                                                                                                                                                                        gene="XYN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               xref="taxon:51453"
                                                     24.8%;
                                  <u>,</u>
                                                     Score 243.6; DB 15; Pred. No. 4.9e-47;
                                    Mismatches 249;
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(XYN2)
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                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola. 1 (bases 1 to 1039)
Dalboege, H. and Hansen, H.P.H.
A novel method for efficient expression cloning of fungal enzy
                                                                                                                                                                                                                                                                                                                                                       endoxylanase; xyll gene.
Humicola insolens
Humicola insolens
                                                                                                                                            Submitted (04-NOV-1993) H. Dalboege, Manager GeneExpress, Novo Nordisk A/S, Symbion, Fruebjergvej 3, 2100 Copenhagen OE, DENM
                                                                                                                                                                                 Dalboege,H.
Direct Submission
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47. .730
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|. . . 1039
                                                                                                          Cocation/Qualifiers
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PLN 18-APR-2005

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RESULT 8
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392; Conserv
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 165436
Sequence
165436
                                                                                                       TACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
                                                                                                                                                                                             CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
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PGGNGYLAVYGWTRNPLYBYYVISSYGTYNPGSQAQYKCTFYTDGDQYDIFVSTRYNQ
PSIDGTRTFQQYWSIRKNKRVGGSVNMQNHFNAWQQHGMPLGQHYYQVVATEGYQSSG
ESDIYYGTH"
47. 103
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/gene="XYL1"
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/EC_number="3.;
/codon_start=1
           from
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RESULT 9
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BD006885
Aspergillus expression sy
BD006885
BD006885.1 GI:18635256
JP 2001025393-A/2.
Humicola insolens
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Berka, R.Michael., Yoder, W., Takagi,
Aspergillus expression system
Patent: US 5667990-A 3 16-SEP-1997;
Location/Qualifiers
1. .1123
                                                                                                                                                                                                                                                                                                                                               CCAGCACTACTACCAGGTCGTCGCCACCGAGGGCTACCAGAGCAGTGGCGAGTCCGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCACGGAATGCCGCT---
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Pred. No. 6.2e-46;
D; Mismatches 210;
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Aspergillus expression system
Patent: JP 2001055393-A 2 30-JAN-2001;
LOVO NORDISK BIOTECH INC
OS Humicola insolens
PN JP 2001025393-A/2
PD 30-JAN-2001 JP 2000185449
PP 17-MAY-2000 JP 2000185449
PR 01-DEC-1993 US 08/161675
PI RANDY M BERKA, WENDY YODER, SHINOBU TAKAGI,
PI CARAPPAN CHETYER BOOMINAZAN
PC C12N15/09, C12N1/15, C12P21/02// (C12N15/09, C12R1: 69), C12N1/15, C12P21/02// (C12N15/09, C12N1/09)
PC (C12N15/09, C12N1/15, C12P21/02// (C12N15/09, C12R1: 69), C12N15/00, C12R1: 66), (C12N15/00, C12R1: 66), (C12N15/00, C12R1: 66), (C12N15/00, C12R1: 69), (C12N15/00, C12R1: 66), (C12N15/00, C12R1: 69), (C12N15/00, C12R1: 66), (C12N15/00, C1
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                                                                                                                      TACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
                                                                                                                                                                                                                                                    CTATACCGACGGCGATCAGTATGACATCTTTGTGAGCACCCGCTACAACCAGCCCAGCAT
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                                      TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT
                                                                                 CTCGGTCAACATGCAGAACCACT
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/mol_type="genomic DNA"
/db_xref="taxon:34413"
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Pred. No. 6.2e-46;
0; Mismatches 210;
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Trichoderma :
AY156910
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Trichoderma sp. SY
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University, 1 Hwayang-Dong, Kwangjin-Gu,
Location/Qualifiers
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Min, S.Y., Kim, B.G. and Ahn, J.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Min,S.Y., Kim,B.G. and Ahn,J.-H. Purification, Characterization, Fungus Trichoderma Strain SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTGCGGCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT
                              CGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGA
                                                                                   CAGAACCATCAACTTCTCCCGGCAGCTACAGCCCCCAACGACAACAGCTACCTCCCGTCTA
                                                                                                                                                                   CAACTGGGCCAACTCGGGCAACTTTGTGGGAGGCAAGGGATGGAACCCGGGCAGCAGCAC
                                                                                                                                                                                                                                                    CTGGAACGACGGCCATGCCGGCGTGACTTACACCAACGGCGCTGGCGGGTCGTTCAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGCCGGCTTTGCCGCTGTTGCCGGAGTCCTGTCGGCTCCTACTGAAGACGTGCAAGT
      CGGCTGGTCCAAGAACCCGGCTCATCGAGTACTACATTGTCGAGAACTTTGGCACCTACAA
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/product="xylanase"
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YLSVYGWSKNPLIEYYIVENFGTYNPSTGATKLGEVTLDGSYYDIYRYGRVNQPSIING
TATFYQYWSVRRSHRSSGSVNVGNHFNAWRNLGLTLGQLDYQIIAVEGYFSSGSANIN
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology & Fermentation Technology of Yunnan, School of Life Science, Yunnan University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma; Trichoderma viride species complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY320048 First 672 bp mRNA linear PLN 14-JUL-2 Trichoderma viride strain YNUCCO183 endo-1,4-beta-xylanase mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and characterization Trichoderma viride YNUCC0183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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GNSYLSVYGWSKNPLIEYYIVENFGTYNPSTGTTKLGEVTSDGSVYDIYRTQRVNQPS
IIGTAAFYQYWSVRRNHRSSGSVTVANHFNAWRNLGLTLGTLDYQIIAVEGYFSSGNA
                                                                                                                                                                                                                     /product="endo-1,4-beta-xylanase"
/protein_id="AAP83925.1"
/db_xref="GI:32481057"
/translation="MYSFTTLLAGFVAVTGVLSAFTENVEVVDVEKRQTIGFGTGFNN
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gtrain="YNUCC0183"
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Score 228.2; DB 15;
Pred. No. 2.2e-43;
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AF246830
                                                                   2 (bases 1 to 2202)
Hera, C., Gomez-Gomez, E. and Roncero, M. Direct Submission 2000) Departamento d Submitted (17-MAR-2000) Departamento d Cordoba, Avda. San Alberto Magno s/n,
                                                                                                                                                                                                                                                                                                                                            Pusarium oxysporum f. sp. lycopersici
Fusarium oxysporum f. sp. lycopersici
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
                                                                                                                                                                                                                          Gomez-Gomez,E., Isabel,M., Roncero,G., Di Pietro,A. and Hera,C. Molecular characterization of a novel endo-beta-1,4-xylanase gefrom the vascular wilt fungus Pusarium oxysporum Curr. Genet. 40 (4), 268-275 (2001)
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  Trichoderma viride mRNA
AJ012718
AJ012718.1 GI:6434132
                                                                               TVI012718
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                                                                                                                                                                                                                                             GGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACG 700
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/gene="xyl5"
/codon_start=1
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/product="xylanase 5 protein"
/protein_ide"AakZ7974.1"
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GFYYSWWSDGADATYTNGEGSSYSMEWKDGGNVGGKGWSPGKARTISYEGEYKPNG
GTQTFQQYWSVRQQHRSTGSVDTGLHFDAWEKAGMKLGTHDYQILATEGYFSSGSSH
MTVSEGASSGGGAGGSTGGDASQCGDDSQQGGDASQGGNGQQGGNGQQGGNGNSFQQPG
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/db_xref="taxon:59765"
/note="forma_specialis: lycopersici"
<686. .>1667
/gene="xy15"
join(<686. .835,883. .1001,1049. .>1
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join(686. .835,883. .1001,1049.
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Trichoderma viride
Trichoderma viride
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Tricoderma viride species complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-NOV-1998) Avni A., University, Tel-Aviv University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furman-Matarasso,N., Cohen,E. and Avni,A. Mutations in the Active Site of the Ethylene Inducing Elicitor Inhibits the b-1-4-Endoxylanase Activity But Elicitation Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avni, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                        CTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCAC
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        AACCTACAACCCATCGACTGGCACCACCAAGCTGGGTGAGGTGACCTCTGACGGCAGCGT
                                                         CACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCAT
                                                                                                             CTCAGTCTATGGCTGGTCCAAGAACCCCCTCATCGAGTACTACATTGTTGAGAACTTTGG
                                                                                                                                                                 TGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGG
                                                                                                                                                                                                                     CAGCAGCTCCAGAGTCATCAACTTCTCTGGCAGCTACAACCCCAACGGCAACAGCTACCT
                                                                                                                                                                                                                                                                   CCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="endo-1,4-beta-xylanase"
/protein_id="CAB60757.1"
/db_xref="G1:6434133"
/db_xref="G1:6434133"
/db_xref="InterPro:IPR001137"
/db_xref="InterPro:IPR001137"
/db_xref="InterPro:IPR001137"
/db_xref="UniProt/TrEMBL:QSUPP"
/db_xref="UniProt/TrEMBL:QSUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:5547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="endo-1,4-beta-xylanase"
/EC_number="3.2.1.8"
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Pred. No. 4.4e-40;
0; Mismatches 341;
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Tel-Aviv, 69978, ISRAEL
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                 The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Dol, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kayai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kayai, J., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Oryza sativa (japonica cultivar-group)
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Ehrhartoideae;
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                                                                                                                                                                                                                                                                                                                                       japonica rice
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Best Local Similarity
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Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Yoshimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Akhmura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Itoh, M., Kagawa, F., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murate, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Session; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,T., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
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                                                                                                                                                                                                             TGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCCAACCTGGAAGGCGGCACCTACGAG
GTGCAGTGGCGCAACACTGGCAACTTCGTCGGTGGGAAGGGAATGGAACCCAGG----AACC
                                                                                                                                                       TGGTGGACCGATGGCGGCGCTCTGCCATATACACCATGGGCGAGGGCTCCAAGTACACT
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/clone="002-168-G08"
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/protein_id="AAV66344 1"

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/db_xref="GI:55824414"

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/translation="MYSERSILLYAVSALTGALARPFDFLDERDGNATSVLBARQVTG
/translation="MYSERSILLYAVSALTGALARPFDFLDERDGNATSVLBARQVTG
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Search completed: February Job time: 5091.94 secs 11, 2006, 20:54:05

Query Match

21

Score

211.4;

DВ 15;

Length

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAT40742 AAT43010 AAS13813 AAD17927 AAQ74098 AAQ94952 ABQ80362 ABQ80364 AAZ28866 AAZ28866 ADK70798 ADK70798 ADL23221 ADJ35015 AAT63044 AAZ6405 AAT63063 AAY29598 AAQ80363 AAQ90363	ID
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ALIGNMENTS

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                                                                                                                                                                                                                                                 Thermomyces lanuginosus.
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                                                                                                                                                                                                                                                                                                                                                          AAT40742;
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                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                   /*tag= a
/product="xylanase"
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Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssochlamus; Paecilomyces; animal feed additive; in-vivo breakdown; cell wall; growth rate; feed conversion; ss

WO9623062-A1.

01-AUG-1996.

26-JAN-1996; 96WO-DK000046.

26-JAN-1995; 95DK-00000094.

(NOVO) NOVO-NORDISK AS

Hansen PK, Wagner P, Muellertz A, Knap IH;

WPI; 1996-454790/45. P-PSDB; AAW01112.

Fungal xylanase prepns. for use as animal feed additives - and DNA construct for producing recombinant Thermomyces xylanase.

Claim 5; Page 45-46; 69pp; English.

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Query Match
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Matches 983
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Pred. No. 5.1e-255;
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                                       The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pyES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS field)
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Humicola lanuginosa; bread; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endo-1,4-beta-D-xylanase
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                                                              TTGTTATTGCTTCGTTGTCTACTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA
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100.0%; Pred. No. 5.1e-255;
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                                                                                                                                                                                                                                                                                                                 The invention relates to a variant xylanase polypeptide (I) or its CC fragment having xylanase activity, comprising one or more amino acid comodifications such that (I) or its fragment has an altered sensitivity to a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or its coding sequence (II) is useful for degrading or modifying plant cell wall or for processing a plant material by contacting the plant cell wall or or for processing a plant material by contacting the plant cell wall or or plant material with (I) or (II). (I) is useful for modifying plant cell wall or processing wood and enhancing the bleaching of wood pulp. (I) is useful for processing wood and enhancing the bleaching of wood pulp. (I) is useful for altering the viscosity derived from the presence of hemicellulose or carabinoxylan in a solution or system comprising plant cell wall material. (C) is useful for preparing a foodstuff such as bread, pretzels, cockies, biscuits or crackers. The present sequence represents the coding sequence of Thermomyces lanuginosus xylanase A as compresent sequence of the invention
                                                                                                                                                                                                               Query Match
Best Local S
Matches 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel variant xylanase polypeptide or its fragment useful for degrading or modifying plant cell wall, comprises amino acid modifications such that the polypeptide has altered sensitivity to xylanase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 64; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-596834/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001; 2001WO-IB000426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylanase A; plant cell wall; baking; cereal; starch production; wood;
wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS13813;
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                                                                                                                                                                                                                 Local Similarity
nes 585; Conserv
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                                                                                                            184
                                                                                                                                                               124 CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC
                                                                           64
                                                                                                                                               4.
                                                                                           GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCCGCACCTACGAGATCAGCTGGGGA
                      GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATC
                                                                                                                                                                                                                                                                                   588 BP; 131 A; 178 C; 168 G; 111 T;
     GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCCAAGAGCCCATC
                                                                           GGTGGAGCGCAGGCCACCTACACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA
                                                                                                                                             CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC
                                                                                                                                                                                                               59.5%; ilarity 100.0%; Conservative
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2000GB-00015751.
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Pred. No. 1.4e-147;
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The invention relates to a Pichia cell comprising at least one copy of heterologous nucleotide sequence encoding a polypeptide of interest, where the codon usage of the sequence has been adjusted to match the preferred codon usage of P. methanolica. The invention also relates to a method for producing high yields of heterologous codon optimised polypeptide in a Pichia cell. The Pichia cell is useful for producing a polypeptide of interest, where the polypeptide is encoded by a nucleotide sequence heterologous to P. methanolica. The present sequence is Thermomyces lanuginosus codon optimised xylanase gene which is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermomyces lanuginosus codon
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                                                                                                                                                                                                                                                     Claim 14; Page 38-39; 61pp; English.
                                                                                                                                                                                                                                                                                                                            Novel Pichia cell useful for producing polypeptide of interest, a copy of heterologous nucleotide sequence encoding polypeptide
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15-MAR-2000;
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                                                                                                                                                                        GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGGCCAGGACAAGCGCACCAGCGGTACC
                                                                                                                                                                                                                                                                                                                           GGCAACAGCTACCTTGCGGTCTACGGTTGGACCCCGCAACCCGCTGGTCGAGTATTACATC
                                                                                                                                                                                                                                                                                                                                                                        GGCTGGAACCCCGGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTTACCAGCCAAAC
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               GTTGCTGACGTGGGCTAA 708
                                                                 CACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC
                                                                                                                  GTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGAC
                                                                                                                                                    GGTACTCAAACTTTCGATCAATATTGGTCTGTTAGACAAGATAAAAGAACTTCTGGTACT
                                                                                                                                                                                                       TGTGATGGTTCTATTTATAGATTAGGTAAAACTACTAGAGTTAATGCACCATCTATTGAT
                                                                                                                                                                                                                             TGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGAC
                                                                                                                                                                                                                                                        GTTGAAAATTTTTGGTACTTATGATCCATCTTCTGGTGCTACTGATTTAGGTACTGTTGAA
                                                                                                                                                                                                                                                                              GTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAG
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                                                                                                                                                                                                                                                                                                                                                          GGTTGGAATCCAGGTTTAAATGCAAGAGCTATTCATTTTGAAGGTGTTTATCAACCAAAT
GTTGCTGATGTTGGTTAA 678
                                                 CATTATTATCAAATTGTTGCAACTGAAGGTTATTTCTCTTCTGGTTATGCTAGAATTACT
                                                                                                   GTTCAAACTGGTTGTCATTTCGATGCTTGGGCTAGAGCTGGTTTGAATGTTAATGGTGAT
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ilarity 72.0%;
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Pred. No. 1.5e-90;
0; Mismatches 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 G;
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Best Local S
Matches 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was isolated from pYES (DSM 6995) and inserted into pH0414 (contg. the TAKA promotter and AMG terminator) to form pAXX-0-1-1-1. This plasmid and pJaL77 (imparting hygromycin B resistance) were used to transform protoplasts of A. foetidus NO953. The xylanase yield was 0.12 g/l. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 35-36; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus foetidus cells expressing heterologous enzyme - partic. fungal lipase or xylanase, provide high yields without significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1993;
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                 567
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                                                                                                                                                            494
                                                                                                                                                                                     387
                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                  327 AAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                     AAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC
                                                                                                                                                          TGTCATCGAGTCGTACGGCACGTACAATCCCGGCAGCCAGGCTCAGTACAAGGGCACATT
                                                                                                                                                                                     CATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGT
                                                                                                                                                                                                                 CCAGGGCAACGGCTACCTGGCCGTCTACGGCTGGACCCCGCAACCCCGCTCGTCGAGTACTA
                                                                                                                                                                                                                                                                                                                                                       CAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                              CTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGGCGCAGGCCACGTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTTCCTCGGGACAACTCGACGGCCCTTCAGGCTCGACAGGTGACCCCCAACGGCGAGGG
TACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
                                           CGACGGCACCCGGACGTTCCAGCAGTACTGGTCTATCCGCAAGAACAAGCATGTCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                         CTGGCACAACGGCTACTTCTACTCGTGGTGGTCCGACGGCGGAGGCCAGGTTCAGTACAC
                                                                  CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
                                                                                                   CTATACCGACGGCGATCAGTATGACATCTTTGTGAGCACCCGCTACAACCAGCCCAGCAT
                                                                                                                              CGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCAT
                                                                                                                                                                                                                                                                          TAAGGGTTGGAACCCGGG---AACCGGCCGCACGATCAACTACGGCGGCTACTTCAACCC
                                                                                                                                                                                                                                                                                                                                 CAACCTCGAGGGCAGCCGCTACCAGGTCAGATGGCGTAACACCCGGCAACTTCGTCGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 239; DB 2;
Pred. No. 5.4e-54;
0; Mismatches 210
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A strain of E. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA fragment is isolated from one of the clones. The sequence of the xylanase gene and protein are given in AAQ94952 and AAR78231 and the gene is deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus japonicus-type cells expressing heterologous protein - esp. fungal enzyme, provide high yields without significant prodn. of protease or mycotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1123
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P-PSDB; AAR78231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 39-40; 50pp; English.
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02-DEC-1995
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CAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGG
                                                                                  CTGGCACAACGGCTACTTCTACTCGTGGTGGTCCGACGGCGGAGGCCAGGTTCAGTACAC
                                                                                                                    CTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACAC
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                                                                                                                                                                                                                                                                                                                     Score 239; DB 2;
Pred. No. 5.4e-54;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; explanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ80362 standard; cDNA;
   WPI; 2003-332729/31
                                                             Jiang B,
                                                                                                                                                                                                                                                 05-AUG-2002; 2002WO-US024842
                                                                                                                                                                                                                                                                                                                                                                           WO2003012071-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. fumigatus
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                                                                                                                             ELITRA PHARM INC.
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                                                             Storms R,
                                                                                                                                                                                          2001US-0309870P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AfXYL1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "Xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 666
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P-PSDB; ABB80185
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beverages, textiles and detergents. Novel isolated Aspergillus fumigatus polypeptide, useful in industries such as those involved in the making of food and

Claim 2; Page 163-64; 169pp; English

CC useful for modulating the amount of cellulose in a composition. Compositions comprising glucose oxidase are useful for modulating the composition. Composition composition composition. Composition composition. Compositions comprising lipase are useful for modulating the amount of lactose in a composition. Compositions comprising lipase are useful for composition The sequences given in ABQ80319-66 encode enzymatic proteins derived fr A. fumigatus. The resulting proteins display the catalytic activity of enzyme such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compounds that comprise a gallate ester linkage in a composition. Compositions comprising cellulase are derived from laccase an

Sequence 666 BP; 142 A; 199 Ç 192 G; 133 T; 0 U; 0 Other;

Similarity

22.8%;

Score 224.6; Pred. No. 3.4

o O

3.4e-50;

DB 10; Length

ð 밁 á 맑 S 문 5 문 Query Match Best Local S Matches 413 181 121 148 13 91 μ 413; ACGAATAACGGCTACTACTACTCCTTCTGGACCGACGGCGGCGAGGTGACCTACACC TGGCACGATGGTTACTACTATTCCTGGTGGAGTGACGGTGGAGGGCGAGGCCACGTACACCC CCCGGCTCGGAGCAATACGTTGAGCTAGCCAAGCCGCAGCTCACCAGCTCTCAGACTGGC ccee---ATGGTCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGGGCCCTTGGCCTTC **AAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCA** AACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGA AAGGGCTGGAACCCGGCC---AGCGAGAAAGCGGTCACCTACAGCGGCTCCTGGCAGACC AACGGCAATGGCGGCCAGTATCAGGTCGACTGGAACAACTGCGGCAACTTTGTTGCTGGG CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGC 0 Mismatches 249; Indels 9; 267 327 120 147 297 240 180 207

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            Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.
                                                                                                                                                    03-AUG-2001; 2001US-0309870P
                                                                                                                                                                            05-AUG-2002;
                                                                                                                                                                                                                                WO2003012071-A2
                                                                                                                                                                                                                                                                                                                       Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                       Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ80364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ80364 standard; cDNA; 705
                                                                                                                             (BLIT-)
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                                                                          2003-332729/31.
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                                                                                                                             ELITRA PHARM
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                                                                                                 Storms R,
                                                                                                                                                                             2002WO-US024842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                        product= "Xylanase
                                                                                                                             INC.
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Claim 2; Page 165-66; 169pp; English.

The sequences given in ABQ80319-66 encode enzymatic proteins derived from CC A. fumigatus. The resulting proteins display the catalytic activity of an CC enzyme such as tannase, cellulase, glucose oxidase, glucosemylase, CC phytase, beta-galactosidases, invertase, lipase, alpha-amylase, CC phytase, beta-galactosidases, invertase, lipase, alpha-amylase, CC polygalacturonase or xylanase. Compositions comprising the tannase are cuseful for modulating the amount of composition comprising comprise a gallate cuseful for modulating the amount of cellulose in a composition. Composition comprising the amount of glucose oxidase are useful for modulating the amount of myo-inositol phosphates in a composition. Compositions comprising comprising glucose oxidase are useful for modulating the amount of myo-inositol phosphates in a composition. Compositions comprising comprising phytase are useful for modulating the amount of compositions comprising beta-galactosidases are useful for modulating the amount of sucrose in a composition. Compositions comprising pha-amylases are useful for modulating the amount of composition. Compositions comprising comprising pha-amylases are useful for modulating the amount of compositions comprising comprising comprising the amount of plyceride in a composition. Compositions comprising comprising comprising the amount of plyceride in a composition. Compositions comprising comprising comprising the amount of plyceride in a composition. Compositions comprising comprising comprising comprising the amount of plyceride in a composition. Compositions comprising comprising comprising comprising comprising composition. Compositions comprising comprising comprising composition. Compositions comprising comprising compositions comprising comprising comprising compositions comprising comprising comprising comprising compositions comprising comprising comprising compositions. Compositions comprising patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A.fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression

Sequence 705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Other;

Query Match Best Local

Similarity

60.5%; 22.7%;

Score 223; DB 10; Pred. No. 9.4e-50;

DB 10;

Length 705,

S 문 S 밁 Ś 맑 S 밁 S 밁 Ś Matches 374 323 263 143 149 269 411; 29 GCAGCTTCAACCCCAGCGGCAÁTGGCTACCTGGCTGTCTÁCGGCTGGÁCCACCAÁCCCCT GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGC GGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCA **ATGGCGCCGGTGGCTCGTACTCCGTCAACTGGAGGAACGTGGGCAACTTTGTCGGTGGAA** ACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAA GGAACAACGGCTACTACTCCTTCTGGACTGATGGCGGCGGCGACGTGACCTACACCA TGATGGTCGGCTTTACCCCCGTTGCCCTTGCGGCCCTTAGCCGCGACTGGGGCCCTGGCCT **AGGGCTGGAACCCTGGAAGCGCTAGGTACCGAGCTTTAAGTAGAACCATCAACTACGGAG** TCAATGAGACTGCTTCATGAGTTCGCTGAGCGCGCCGGCACCCCAAGCTCCACCGGCT TGCTGGCGTGCTCCGCCATTGGAGCTCTGGCTGCCCCCGTCGAACCCCGAGACCACCTCGT Conservative <u>.</u> Mismatches 250; CGGCCTGAACGCAAGAGCCATCCACTTTGAGG Indels 18; Gaps 268 142 82 262

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RRESULT 9
AAZZ886 A
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pulp-bleaching; ds.
This sequence corresponds to a degenerate sequence encoding a xylanase precursor from Streptomyces olivaceoviridis. The sequence can be insert into the plasmid pQE60 to generate plasmid PERM P-16713 for expression e.g. E.coli. The xylanase is useful for the preparation of xylo-
                                                                                                         Claim 1;
                                                                                                                                                 A xylanase gene, pulp-bleaching.
                                                                                                                                                                                                                                    WPI; 1999-613780/53
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01-FEB-2000
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SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
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418. .:
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2003 to correct OS field.)
                                                                                                  xylanase; plasmid; expression;
pulp-bleaching; ds.
        sig_peptide
                                                                                 Streptomyces
                                                                                                                                   Streptomyces
                                                                                                                                                       27-AUG-2003
01-FEB-2000
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                                                                                                                                                                                                                                                                                                                                             TCCAAGCGGACCGGCACCATCACCACCGGCAACCACTTCGACGCCTGGGCCCGCTAC
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                                                                                                                                                                                                                                                            AGCGGCTCCTCCAACCTCACGGT
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                                                                                 olivaceoviridis
                                                                                                                                    olivaceoviridis
                                                                                                                                                       (revised)
(first entry)
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     /*tag= a
/gene= "XynG"
/product= "xyl
298. .417
                                                             Location/Qualifiers
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                    "xylanase"
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D; Mismatches
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                                                                                                                                   xylanase
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                                                                                                              E.coli;
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                                                                                                                                   (XynG)
                                                                                                              xylo-oligosaccharide; xylan;
                                                                                                                                   gene
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1195 BP; 230 A; 457 C; 333 G; 175 T; 0
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P-PSDB; AAY44183.
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SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU
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AGCGGCTATGCTCGCATCACCGT 692
                                                                                  GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
                                                                                                                                       TCCAAGCGGACCGGCGCACCATCACCACCGGCAACCACTTCGACGCCTGGGCCCGCTAC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes the Streptomyces olivaceoviridis xylan enzyme. The xylan enzyme has good heat stability, high activity under acidic and neutral pH. The xylan enzyme can be used as a feed additive and can be widely used in animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-resisting, antiproteinase acidic-neutral
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                             TCGGGCAGCTTCTACCCGTCCGGCAACGGCTACCTGGCGCTGTACGGGTGGACCTCGAAC
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30-AUG-2002;
03-SEP-2002;
03-SEP-2002;
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Wagner C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; A. niger; (hemi)cellulase; filamentous fungus; dough; bread; biscuit; elasticity; stability; stickiness; extensibility; machinability; crumb structure; softness; flavour.
This sequence encodes an A. niger (hemi)cellulase NBE021. The (hemi)cellulase coding sequences of the invention are derived from a filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase
                                                                                            Disclosure; SEQ ID
                                                                                                                                                             Novel hemicellulase NBE012, NBE derived from Aspergillus niger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2003;
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DB; ADL23222.
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Best Local Similarity
Matches 398; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in producing dough, which is useful for preparing a baked product such as bread, biscuits from the dough. Fragments of the (hemi)cellulase DNA are useful as probes and primers for detecting the expression of (hemi)cellulose mRNA in a biological sample such as a tissue. They are also useful as query sequences to identified other family members or related sequences. Anti-(hemi)cellulase antibodies are useful for qualitative or quantitative determination of a polypeptide in a biological sample. These antibodies are also useful in diagnosing organism is infected with Aspergillus. The dough prepared by using the inventive (hemi)cellulase has increased strength, elasticity, stability, reduced stickiness, improved extensibility and machinability. The prepared baked product has improved crumb structure, softness and flavour. The (hemi)cellulase has higher specificity towards the substrate, is less antigenic and produces less undesirable side
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Pred. No. 2.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lightn reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
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Pred. No. 4.5e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             258; Indels
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                                                          Identifying DNA fragments encoding proteins, e.g. for new enzyme discovery - by direct screening of a cDNA library in bacteria transformed with DNA from eukaryotic organism producing the protein.
                                                                                                                                                                                                                  17-APR-1997
                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2003
22-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                    AAT63044;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAT63044 standard;
                                                                                                                                                                         13-OCT-1995;
                                                                                                                                                                                             14-OCT-1996;
                                                                                                                                                                                                                                     WO9713853-A2
                                                                                                                                                                                                                                                                                              Aspergillus
                                                                                                                                                                                                                                                                                                                              Endoxylanase;
                                                                                                                                                                                                                                                                                                                                                  Aspergillus niger xylanase cDNA
                                                                                                                                                    (KONN)
                                                                                                                                Den Broeck HC,
                                                                                                   1997-235889/21.
DB; AAW14597.
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                                                                                                                                                                                                                                                                                                                  screening;
                                                                                                                                                    GIST-BROCADES
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                                                                                                                                                                                                                                                                                              niger; strain N400 (CBS120.49)
                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                             xylanase; protein detection; enzyme
                                                                                                                                                                         95EP-00202777
                                                                                                                                                                                             96WO-EP004510
                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                           Location/Qualifiers
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A cDNA clone (AAT63044), deposited as CBS 590.95, codes for a xylanase (AAW14597) of Aspergillus niger N400 (CBS120.49). It was isolated using a method for identifying a DNA fragment encoding a protein of interest. The

6; Page 19-20; 30pp;

English.

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Best Local
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                                                                                                                                         16-OCT-2003
25-MAR-2003
28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      method involves the direct screening of a cDNA library prepd. in bacteria (e.g. E. coli) transformed with DNA from a eukaryotic organism (e.g. A. niger) that produces the protein. Screening for xylanase-producing clones can be performed on agar plates containing oat spelt xylan and RBB-xylan. The method was utilised in the identification of cDNA clones (AAT63042-46) coding for A. niger cellulase, xylanase and arabinoxylan degrading enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;
                Nonomuraea flexuosa
                                            Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin; thermostable; biobleaching; wood pulp; bleaching; hemicellulase; paper processing; hemicellulose; ss.
                                                                                                           Actinomadura
                                                                                                                                                                                                                                     AAX90405 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                              CTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCACGTACAAGGGCÁCCGTCACCTCGGÁCGGATCCGTTTTÁCGATATCTACACGGCTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTC
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                                                                                                                                       (revised)
(revised)
(first en
                                                                                                         вp.
                                                                                                         DSM43186 35 kDa xylanase encoding
                                                                                                                                                                                                                                         DNA; 1375
                                                                                                                                         entry)
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Pred. No. 2.1e-43;
                                                                                                                                                                                                                                         ВP
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                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                     717
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AAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCT 274

CGGGCGGCAGCTACAGCACCTCGTGGCGGAACACCCGGGAACTTCGTCGCCGGCAAGGGCT

588

155 469

TGCTGCCCGGCACGGCCCACGCCGACACCACCACCACCACCCAGACCCAGACCAGACCAGCCAGCCCAACCTGG
ATGGTTATTACTATTCCTGGTGGAGTGACGGTGAGGCGCAGGCCACGTACACCAACCTGG

468 214

ACGGCTACTTCTACTCGTTCTGGACCGACGCGCCCGGGACCGTCTCCATGACCCTCCACT

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The present invention describes a culture medium obtained from the culture of a recombinant host cell that is not Actinomadura flexuosa and characteristic content of a recombinant host cell that is not Actinomadura flexuosa and content in the protein comprises an amino acid sequence from a cylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481. Chalso described is an enzyme preparation derived from the culture medium. Characteristic composition can be used in a method for biobleaching, composition can be used in a method for biobleaching. Characteristic content in pulp and paper processing. The xylanases are hemicelhulases characteristic content of wood pulp, increase its drainability or decrease its water content of wood pulp, increase its drainability or decrease its water content of wood pulp, increase its drainability or decrease its water content of wood pulp, increase its drainability or decrease its water content of wood pulp, increase its drainability or decrease its water content of wood pulp, increase its drainability or decrease its water consumption of biobleaching of wood pulp reducing the caned to accidify the pulp prior to xylanase have a pH optimum and content of the content of the medical prior to xylanase the content of the consumption of bleaching chemicals reducing the formation of partially degrade the hemicellulose in wood pulp which enhances the extractability of lignins by conventional bleaching chemicals and results in lower consumption of bleaching chemicals reducing the formation of consumption of bleaching chemicals reducing the formation of services and results in lower consumption of bleaching chemicals reducing the formation of consumption of bleaching chemicals reducing the formation of services and results in the consumption of bleaching chemicals reducing the formation of consumption of bleaching chemicals reducing the formation of consumption of bleaching chemicals reducing the formation of consumptions of the consumption of bleaching chemicals reducing the fo
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1994;
31-OCT-1994;
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                                                                                                                                                                                                                Sequence
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                                                                                                                                 403;
                                                                                                                                                                                                                1375
        CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACG 154
                                                 TCGGCCTCCGGCGCATCGTCACCAGTGCCTTCGCCCTGGCACTCGCCATCGCCGGTGCGC 408
                                                                                      TCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGG 94
                                                                                                                                 Conservative
                                                                                                                                                                                                                BP; 265 A; 517 C; 400
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94US-00332412.
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                                                                                                                                                  20.1%;
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                                                                                                                                 <u>.</u>
                                                                                                                                                    Score 197.2; DB 2
Pred. No. 1.1e-42;
                                                                                                                                   Mismatches 273;
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Search completed: February 11, 2006, 18:30:52 Job time: 619.413 secs

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ALIGNMENTS

JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 DR637934 REFERENCE FEATURES DEFINITION POCUS TITLE AUTHORS source Gibberella moniliformis Gibberella moniliformis Gibberella moniliformis Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Bukaryota; Fungi; Ascomycota; Pezizomycotina; Gibberella. Email: browndw@ncaur.usda.gov TIGR sequence name: FVMB275TH Seq primer: AAT TAA CCC TCA CTA 1815 N. University Tel: 309 681 6230 Fax: 309 681 6689 Contact: Brown USDA/ARS/NCAUR Unpublished (2005) Contact: Brown, D.W. 1 (bases 1 to 860) Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster EST DR637934 860 bp mRNA linear EST 11-JUL-2005 EST1028559 FvM Gibberella moniliformis cDNA clone FVMB275, mRNA DR637934.1 GI:70712768 /tissue_type="mycelia" /clone_Tib="FVM" /clone_Tib="FVM" /clone_Tib="FVM" /clone_Tib="FVM" /clone_Tib="FVM" /note="Vector: pambueScript II SK(+) XR; Site_1: EcoRI; /note="Vector: pambueScript II SK(/db_xref="taxon:117187" /clone="FVMB275" /organism="Gibberella /mol_type="mRNA" /strain="m3125" ocation/Qualifiers . 860 St, Peoria, moniliformis" Ħ AAG 61604, ନ୍ଧ USA Library

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Gibberella moniliformis

Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 883)

1 (bases 1 to 883)

Brown, D.W., Cheung, F., Procttor, R.H., Butchko, A.E., Zheng, L., Lee, Y.
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Kandra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                             DR643290
EST1033915
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Pred. No. 3.6e-71;
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Tel: 309 681 62
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Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.
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                        CTTCGACGCCTGGGAGAAGGCTGGTATGAAGCT---CGGTACCCACGACTACCAGATCCT
                                                                                               GCAGTACTGGTCTGTTCGCCAGCAGCATCGCTCTACTGGTAGCGTTGACACTGGTCTTCA
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R sequence name: FVMCX47TH
primer: AAT TAA CCC TCA C
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nilarity 67.4%;
Conservative
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/tissue type="mycelia"
/clone lib="FMM"
/clone lib="FMM"
/clone lib="FMM"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/site 2: XhoI; anamorph: Fusarium verticillioldes. Library
FVM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlabad CA) at
approximately 1 g mycella per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
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/mol_type="mRNA"
/strain="m3125"
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1 (bases 1 to 882)

Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S Generation of ESTs from late blight-challenged potato tubers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Canadian Potato Genome Project 921 College Hill Rd, Fredericton, (Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Barry Flinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum (potato)
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                                                                                                                                                                 TGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGG 703
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AAGGCCGGTGGAGATACTCCCTGACCTGGAGCGGCAACGGCAACGTCGTTGCTGGAAAG
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                              /clone lib="Late Blight-Challenged Tubers"
/notes "Vector: pBluescript II SK(+) XR, Site 1: BooRI;
/notes "Vector: pBluescript II SK(+) XR, Site 1: BooRI;
Site 2: XhoI; supplier: Fathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Tubers"
/lab_host="XL10-Gold"
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/clone="49478"
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/cultivar="Shepody"
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Pred. No. 1.1e-56;
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GTTGGATCCGGTGGC
                                                  GTTGCTGACGTGGGC 705
                                                                                                                                      CACAACTACCAGATTGTTGCTTCCGAGGGTTACCACAGCAGCGGTTCCGCCGATATCACT 678
                                                                                                                                                                                        CACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC 690
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49478 5', mRNA sequence.
DN588726
DN588726.1 GI:61239134
EST.
Solanum tuberosum (potato)
Solanum tuberosum The Canadian Potato Genome Project 921 College Hill Rd, Fredericton, C Email: bflinn@bioatlantech.nb.ca 1 (bases 1 to 675)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., D., Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and R., Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and R., Generation of ESTs from late blight-challenged potato tubers Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum. DN588726 675 bp mRNA linear EST 15-MAR-200: 49478.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone Contact: Barry Flinn Unpublished (2005) primer: T3. /lab_host="XL10-Gold"
/clone lib="Late Blight-Challenged Tubers"
/clone lib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future /cultivar="Shepody"
/db_xref="taxon:4113"
/clone="49478" tissue_type="Tubers" organism="Solanum tuberosum" location/Qualifiers . 675 _type="mRNA" Š BioAtlantech E3B CANADA EST 15-MAR-2005 Regan, S

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ACCESSION
VERSION
KEYWORDS
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CF867983
                                                                                                                                                                                                  TOCUS
                                             REFERENCE
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                                                                                                                                                                  CF867983 744 bp mRNA tric013xe09.bl T.reesei mycelial culture, Hypocrea jecorina cDNA clone tric013xe09,
              Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek Teunissen, P.J.M., van Solingen, P., Dankmeyer, L.,
                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreales;
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                                         (bases 1 to 744)
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No. 8.9e-55;
                                                                                                          Trichoderma
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Version 6 October
mRNA sequence.
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Hypocrea.
                 Mitchell, T.K.,
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Mismatches

Indels

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Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Ralph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEMS Microbiol. Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 919-513-0024
                                                                                                                                                                                                                                                                                                                                                                il: ralph_dean@ncsu.edu
primer: LT-F1 primer:
Location/Qualifiers
                                                                                     /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                          /clone="tric013xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture,
                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                                                                                                                                                                     organism="Hypocrea
                                                                                                                                                                                                                                                   db_xref="taxon:51453"
23.3%;
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Score 229; DB 7;
Pred. No. 1.6e-53;
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AGGTCGAATCCGTGGCTGTGGAGAAGCGCCAGACGATTCAGGCCGGCACGGGCTACAACA CCGGCGGCAGTTCTCCGTCAACTGGTCCAACTCGGGCAACTTTGTCGGCGGCAAGGGAT AAGGCGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCT CAGGGAATGCCACGGAGCTCGAAAAGCGACACACACCCCCAACTCGGAGGGCTGGCACG ACGGCTACTTCTACTCGTACTGGAACGATGGCCACGGCGCGTGACGTACACCAATGGTC ATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCTAGACCTGG TCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGGGGCCCTTGGCCTTCCCGG ACTACCAGATCGTTG-CAACGGAGGGCTACTTCAGCAGCGGCTATGCTC ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCA AGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCG ACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCCTGATCGAGTACTACATCGTCG ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCG GGCAGCCCGGCACCAAGAACAAGGTCATCAACTTCTCGGGCAGCTACAACCCCCAACGGCA GGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCA reaccirectedeceses de la reconstructe de la reconst ACACGGCGAACCACTTCAACGCGTGGGCTCAGCAAGGCCTGACGCT--AGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACT CCGCCACCTTTTACCAGTACTGGTCCGTCCGCCGCAACCACCGCTCGAGCGGCTCCGTCA CCCAMACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC **ACGGCAGCGTCTACGACATTTACCGCÁCGCAGCGCGTCÁACCAGCCGTCCÁTCATCGGCA** AGAACTTTGGCACCTACAACCCGTCCACGGGCGCCCACCAAGCTGGGCGAGGTCACCTCCG 0 CGGGACGATGG 682 4. 215 155 635 454 394 395 334 335 274 275 154 692 574 575 514 515 455

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB898036 799 bp mRNA linear EST 02-JUL-
tric013xe09 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric013xe09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Pamela K. Foreman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                   ACAGCTACCTTGCGGTCTACGGTTGGACCCGCCAACCCCGCTGGTCGAGTATTACATCGTCG
                                                                                                                                                                   CCGGCGGCAGTTCTCCGTCAACTGGTCCAACTCGGGCAACTTTGTCGGCGGCAAGGGAT
                                                                                                                                                                                                          AAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCT
                                                                                                                                                                                                                                                                                                                            AGGTCGAATCCGTGGCTGTGGAGAAGCGCCAGACGATTCAGGCCGGCACGGGCTACAACA
                                                                                                                                                                                                                                                                                                                                                                 CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACG 154
                                                                                    GGCAGCCCGGCACCAAGAACAAGGTCATCAACTTCTCGGGCAGCTACAACCCCAACGGCA
          ACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCCTGATCGAGTACTACATCGTCG
                                                                                                                                                                                                                                                                                   ATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (650) 846-7635
(650) 621-7817
L: Pforeman@genencor.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="mycelia" //dev_stage="mycelia" //dev_stage="mycelia" //deve_tor: pREP3Y; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
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Pred. No. 1.6e-53;
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                                                                                                                                                                                                                                                                                                       Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
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EST.
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/db_xref="taxon:4558"
/clome="QXI_9_D10_A002"
/lab host="DH10B-T1 phage-resistant E. coli"
/lab host="DH10B-T1 phage-resistant E. coli"
/clome_lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
xhoi; Site_2: Xhoi; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                  organism="Sorghum bicolor"
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748 ATTACCAGATTGTTGCCGTGGGAGGGTTACTTTAGCTCTGGCTCTGCTC
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Other_ESTs: OX1_9_
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Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                 Tel: 706 542 1860 Fax: 706 583 0210
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                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 639)
Brown, D. W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster unpublished (2005)
                                                                                                                                                                                                                                                         sequence.
DR624928
Contact: Brown USDA/ARS/NCAUR
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EST1015056
                                                                                                                                                                                     Gibberella
                                                                                                                                                                                                         Gibberella moniliformis
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                                                                                                                                                                                                                                                                                             FvI Gibberella
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                                                                                                                                                                                                                                           GI:70699610
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Pred. No. 1.1e-51;
0; Mismatches 209;
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moniliformis
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                                 CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT--
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TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTT
                                                                  GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
                                                                                                     TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGGCGCTGTCAACATGCAGA
                                                                                                                                     TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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Indels

6,

Gaps

143 223 83

283

500

583 440

557

380 463 320 403 343

203

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1815 N. University St, Peoria, IL
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIBBOSTH
Seq primer: AAT TAA CCC TCA CTA AJ
Location/Qualifiers
                                                                                                                        FVI was prepared from growth on excised maize seedling roots and shoots. The roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 1066 conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIZOl Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOL The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit, Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mycelia"
/clone_Tib="FvI"
/clone_Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Libr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Gibberella"
Score 220.4; DB 8; Pred. No. 4.3e-51;
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 749)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, 1 Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIAM22TH
Seq primer: AAT TAA CCC TCA CTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR623097 749 bp mRNA linear EST1013225 FvI Gibberella moniliformis cDNA clone
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                                   CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG 283
                                                                                                             ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCCTGGAAGGCGGCA 223
ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
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309 681 6689
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/clone_lib="FvI"
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mol_type="mRNA"
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|strain="m3125"
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Plattner,R.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 768)
Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,
Mard, M. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 bp mRNA tric033xj11.b1 T.reesei mycelial culture, Hypocrea jecorina cDNA clone tric083xj11, CP881056
                                                                                                                                                                                                                                       Email: ralph dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     North Carolina State University Campus Box 7251, Raleigh, NC 27/Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                               Contact: Ralph A. Dean Fungal Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterization of the protein processing and secretion in a comprehensive set of expressed sequence tags from Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                       Fax: 919-513-0024
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                               /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
               and Nitrogen sources and concentrations."
                                                                                   /db_xref="taxon:51453"
/clone="tric083xj11"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
                                                                                                                                                                                   organism="Hypocrea jecorina"
/mol_type="mRNA"
                                                                                                                                                                   strain="QM6a"
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                                                                                                                                                                                                                                                                      CB907827 822 bp mRNA linear EST 02-JUL-: tric083xj11 T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tric083xj11, mRNA sequence. CB907827 CB907827 CB907827.1 GI:30122485
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G. Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of biomass-degrading enzymes in filamentous fungus Trichoderma reseei J. Biol. Chem. 278 (34), 31988-31997 (2003)
                                                                                                                                                      Hypocrea jecorina (anamorph: Trichoderma reese Hypocrea jecorina Hypocrea jecorina Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreaceae; 1 (bases 1 to 822)
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Best Local Similarity
Matches 407; Conserv
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Contact: Pamela K. Foreman
Genencor Intl
925 Page Mill Road, Palo Alto,
925 Page 1650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
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           GCTAAGGGGGCT
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                                                   CTGACGTGGGCT
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/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="tric083xj11"
/dev_stage="mycelia"
/clone_lib="T.reesi mycelial culture, Version 3 april"
/clone_lib="T.reesi mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r: LT-F1 primer.
Location/Qualifiers
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ed. No. 6e-51;
Mismatches 261;
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Best Local
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 686)

1 (bases 1 to 686)

Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Yuterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D., Kendra,D.F., Town,C.D. and Whitelaw,C. tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D.W.

Tenna/are/McAnter
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Similarity 63.2%;
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GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTTACCAGCCAAACGGCAACGGCTACC
                                                                                                         CCTACGAGATCAGCTGGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                                                                                                                                                                    ACTATTCCTGGTGGAGTGACGGTGGAGCCGCAGGCCACGTACACCAACCTGGAAGGCGGCA
                                                                                                                                                                                                                                                                                                                           CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 163
                                                                            ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
                                                                                                                                                                           TCTACTCTTGGTGGTCTGATGGTGGTGGCCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                                                                                                                                                                                                        CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11: browndw@ncaur.usda.gov
R sequence name: FVIB801TH
primer: AAT TAA CCC TCA CTA AAG
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309 681 6230
309 681 6689
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/clone_Tib="FVI"
/clone_Tib="FVI"
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI, anamorph: Fusarium verticillioides. Library
FVI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The CDNA was directionally ligated into the palueScript II SK(+) XR vector (cDNA Synthesis Kit, Stratagene)."
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/clone="FVIB801"
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FvI Gibberella moniliformis cDNA clone FVIB801,
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                                                                                                                                                                                                                                                                                                                                                                      Score 219.4; DB 8;
Pred. No. 8.5e-51;
0; Mismatches 211;
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RESULT 13
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, 1
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIEA21TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Brown, USDA/ARS/NCAUR
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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EST1021648 FvI Gibberella moniliformis cDNA clone FVIEA21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 309 681 6230
Fax: 309 681 6689
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/note="Westor: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
                                                                                                                                                                                                                                                                                                                                organism="Gibberella
/mol_type="mRNA"
                                                                                                                                                                                                                 /tissue_type="mycelia"
/clone_lib="FvI"
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/clone="FVIEA21"
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                                   Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
            spliced introns in multiple genes of the Unpublished (2005) Contact: Brown, D.W.
                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; C (bases 1 to 733)
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                            CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGGAACCACTACTATCAGA
 TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
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Query Match
Best Local Similarity
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1815 N. University
Tel: 309 681 6230
Fax: 309 681 6689
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TIGR sequence name: FVIDX40TH
Seq primer: AAT TAA CCC TCA C
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GCCACTTCGACGCCTGGGCTGGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
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                                                                    TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGGCGCTGTCAACATGCAGA
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/clone lib="FvI"
/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/site 2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlabad CA) at
approximately 1 gmycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (CDNA Synthesis Kit; Stratagene)."
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/clone="FVIDX40"
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Pred. No. 8.6e-51;
0; Mismatches 211;
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REFERENCE
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                                                 224 CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG 283
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Tel:
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Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB280TH
Seq primer: AAT TAA CCC TCA CTA AAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 739)
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                                                                                                                                                                                                   CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT 178
ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
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                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 / Clone Libs FYI / Clone / Libs FYI / Inotes Wector: pBlueScript II SK(+) XR; Site 1: EcoRI; // Inotes Wector: pBlueScript II SK(+) XR; Site 2: XhoI; anamorph: Fusarium verticillioTdes. Library FYI was prepared from growth on excised maize seedling roots and shoots. The roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 10e6 conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIZOl Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOl. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:117187"
/clone="FVIB280"
/tissue_type="mycelia"
/clone_lib="FVI"
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/strain="m3125"
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                                                                                                   IGGTGGTCTGATGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC
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                                      CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA
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                                                                      GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 643
                                                                                                                                         TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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                                                                                                                                                                                                          TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT 523
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     TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                                         TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGCGCTGTCAACATGCAGA 595
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Search completed: February 11, 2006, 20:39:40
Job time : 4981.03 secs

653

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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(c) 1993 - 2006 Biocceleration Ltd
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Sequence 1, Appl1	Sequence 2, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 46, Appl	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	•	Sequence 4, Appli	Sequence 5, Appli	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

RESULT 1 US-08-886-765-1 TELEPHONE: 212-867-0123 TELEPAX: 212-878-9655 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 983 base pairs Sequence 1, Application US/08886765 Patent No. 5817500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IIBM Compatible COMPUTER: IIBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/886,765 FILING DATE: 1-JUL-1997 CLASSIFICATION: 435 CLASSIFICATION: 435 GENERAL INFORMATION: MOLECULE TYPE: CI ORIGINAL SOURCE: ORGANISM: Ther ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 4324.204-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 APPLICANT: Hansen, Peter Kamp APPLICANT: Wagner, Peter APPLICANT: Mullertz, Anette APPLICANT: Knap, Inge Helmer TITLE OF INVENTION: Animal Feed Additives NUMBER OF SEQUENCES: 2 FEATURE: CORRESPONDENCE ADDRESS: ADDRESSEE: No. 58175000 No. 5817500disk of No. 5817500th America, Inc. STREET: 405 Lexington Avenue STREET: 405 Lex CITY: New York STATE: NY ORGANISM: Thermomyces lanuginosus STRAIN: DSM 4109 LENGTH: 983 base pairs TYPB: nucleic acid STRANDEDNESS: single COUNTRY: U: ZIP: 10174 TOPOLOGY: USA linear CDNA

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US-09-115-660-1
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APPLICATION UNMBER: 08/886,765
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
REFERENCE/DOCKET NUMBER: 4324.204-US
TELEPHONE: 212-867-0123
TELEPAN: 212-867-0123
TELEPAN: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
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Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 983; Conservative 0
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CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
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Pred. No. 3.6e-269;
); Mismatches 0;
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Dequence 3, Application US/08458023B

Patent No. 5667990

GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Takegi, Shinobu

APPLICANT: Boominathan, Karuppan C.

TITLE OF INVENTION: ASPERGILLUS EXPR.

NUMBER OF BEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5667000
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-458-023B-3
STREET: 405 Lexington
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACHENT TYPE: 11
ORIGINAL SOURCE:
ORGANISM: Humic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMB: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/458,023B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 1.1e-57;
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RESULT 4
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US-08-468-812-1
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                                                                                                                                   Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: not relevational relevations of the state of the s
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LPPLICANT: Paloheimo, Marja
LPPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: Of Use
TITLE OF REQUENCES: 25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-UUL-1994
CLASSIFICATION: 435
ATTORNEY JOACHT
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APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0: FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Y: U.S.A.
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Pred. No. 9.1e-46;
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Patent No. 630011
COUNTA:

ZIP: 2005
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TWOTTEN: PC-DOS/MS-DOS
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APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACGTGGGCTAAGACGTAACCTGGTG 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGGGGAACGTACGACATCTACGAGACCTGGCGGTACAACGCGCCGTCCATCGAGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGCTGGGGCACCTACCGGCCCACC-----GGCACCTACAAGGGCACCGTCACCACCG
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                                                                                                                                                                                                                                                                                                                     E: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vehmaanper , Jari
Fagerstr m, Richard
Lantto, Raija
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M ntyl , Arja
                                                                                                                                                                                                                                                                                                                     KESSLER, GOLDSTEIN & FOX, P.L.L.C. ork Ave., N.W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Secretion of
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-CCTGGGCAGCCACG

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CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

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TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAMB: BUGA18Ky, Lawrence B.
REGISTRATION NUMBER: 35,086
REGISTRATION NUMBER: 1050
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
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APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-OCT CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                529 CGGGCGGCAGCTACAGCACCTCGTGGCGGAACACCGGGAACTTCGTCGCCGGCAAGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                          215 AAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 ATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGG 214
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CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC 574
                                                                                                                                                                   AGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCG
                                                                                                                                                                                                                                                                                              GGTCCACCGG---GGGACGGCGGACCGTGACCTACAACGCCTCCTTCAACCCCGTCGGGTA
                                                                                                                                                                                                                                                                                                                                      GGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCA 334
                                         ACGGGGGAACGTACGACATCTACGAGACCTGGCGGTACAACGCGCCGTCCATCGAGGGCA
                                                                                 ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCA 514
                                                                                                                             AGAGCTGGGGCACCTACCGGCCCACC-----GGCACCTACAAGGGCACCGTCACCACCG
                                                                                                                                                                                                             ACGGCTACCTCACGCTCTACGGCTGGACCAGGAACCCGCTCGTCGAGTACTACATCGTCG
                                                                                                                                                                                                                                                    ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGCTACTTCTACTCGTTCTGGACCGACGCGCCCGGGACCGTCTCCATGACCCTCCACT 528
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Pred. No. 9.1e-46;
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GENERAL INFORMATION:
                                                                                                                                             TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                        PILING LAND CRASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
APPLICATION NUMBER: 31-OCT-1994
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BUGAISKY, Lawrence B.
REGISTRATION NUMBER: 35,086
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STREET: Washington
STATE: D.C.
T S.A.
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 29-JUL-1994
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF
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                                     TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
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                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEB: STERNE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   997
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                                                                        nucleic acid
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INVENTION: Production
F SEQUENCES: 39
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                                                                                                     1375 base pairs
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Suominen, Pirkko
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Fagerstr m, Richard
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                                       linear
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                                                       ŏ.
                 DNA (genomic)
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US-08-590-563-1

MOLECULE TYPE: NAME/KEY: LOCATION:

Best Local Similarity

Query Match

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; NAME/KEY:
; LOCATION:
US-09-770-621-1
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US-09-235-832-1
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Best Local Similarity 58.6%;
                                                                                                                                                                                                Sequence 1, Application US/09235832 Patent No. 6667170
                                           APPLICANT: M ntyl, Arja
APPLICANT: Vehmaanper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Lantto, Raija
APPLICANT: Suominen, Marja
APPLICANT: Suominen, Tarja
APPLICANT: Lahtinen, Tarja
APPLICANT: Lahtinen, Tarja
                                                                                                                                                                                  GENERAL INFORMATION:
             NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
 ADDRESSEE:
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Pred. No. 9.1e-46;
0; Mismatches 273;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKST NUMBER: 1050.0340003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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LENGTH: 1375 base pairs
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CITY: W
STATE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/235,832
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 AGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCG
                                                         ACAGCTACCTTGCGGTCTACGGTTGGACCCGGCAACCCGCTGGTCGAGTATTACATCGTCG
                                                                                                    GGTCCACCGG---
                                                                                                                                   GGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCA
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Pred. No. 9.1e-46;
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Indels Length 1375;

12;

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408 154

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APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, KAORU
APPLICANT: MUNAKAMI, KAORU
APPLICANT: MUNAKAMI, TAKESHI
ITILE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh1 GENES ORIGINATING
ITILE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
ITILE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(MMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT APPLICATION OR: 52
SOFTWARE: PATENTING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 822
TYPE: DNA
ORGANISM: TRICHODERMA VIRIDE MC300-1
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                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (41:
US-09-254-733-8
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US-09-254-733-8
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                                                                              Query Match 19.8%;
Best Local Similarity 69.0%;
Matches 281; Conservative
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                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: CDS
LOCATION: (14)
                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: mat_peptide
LOCATION: (113)..(809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE: Sig_peptide LOCATION: (14)...(112)
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o. 6277596
    CTGAAAACAAGGGTCATCAACTTCTCGGGCACCTACAACCCCAACGGCAACAGCTACCTC
                              CTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTTACCAGCCAAAACGGCAACAGCTACCTT 345
                                                                                                                                                                                                                                  intron
(286)..(412)
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(113)..(285)
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                                                                          Score 194.2; DB 3;
Pred. No. 5.1e-45;
0; Mismatches 123;
                                                                                                              Length
                                                                              Indels
                                                                                                                   822;
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US-08-121-436A-1
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Sequence 1, App
                                                    PILING DATE: 18-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F193/00221

FILING DATE: 24-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893

PRIOR APPLICATION NUMBER: US 07/524,308

FILING DATE: 29-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308

PILING DATE: 16-MAY-1990

ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFOR
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/121,430
FILING DATE: 16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
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1100 New York Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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Saarelainen, Ritva
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; LOCATION:
US-08-121-436A-1
                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application
; Patent No. 6228629
; GENERAL INFORMATION:
APPLICANT: PALOHEII
; APPLICANT: HAKOLA,
; APPLICANT: M. NTYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-768-373-1
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING STORTM: Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 278; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOSTREET: 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                   APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                    WASHINGTON
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VEHMAANPER , JARI
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llarity 68.5%;
Conservative
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Pred. No. 8.8e-44;
0; Mismatches 125; Indels
                                                                                                                                                                                                    GOLDSTEIN & FOX,
E, SUITE 600
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                                                #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2840
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: exon

1.1039
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FILING DATE: 18-DEC-1995
PRIOR APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 195..42:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: CBS730.95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 283; Conserv
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                                                               835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 AAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC 326
895
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                                                                                         TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT
                                                                                                                                                        TACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
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CAATGTTGGCGGC
                               CACCGTTGCTGAC 699
                                                               TTCCCATGATTATCAGATTGTGGCTACTGAGGGTTACTACTCGTCTGGCTCGGCGACTGT
                                                                                                                                CGAGGGCACCAAGACCTTCTACCAATACTGGTCTGTGCGCACCTCCAAGCGGCACCGGCGG
                                                                                                                                                                                                                                    CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
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907
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Pred. No. 2.1e-41;
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834 626 777 995 717

RESULT 11 US-09-849-242A-1

Sequence 1, Application US/09849242A Patent No. 6635464
GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA

MONTYLO, ARJA VEHMAANPERO, JARI

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NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /k
SEQUENCE DESCRIPTION: SEQ
US-09-849-242A-1
8
                                        Query Match 18.5
Best Local Similarity 65.4
Matches 283; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/ACENT_IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                              FEATURE:
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TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
267 ANAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC 326
                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  STRAIN: CBS730.95
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TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Chaetomium thermophilum
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LAHTINEN, TARJA
FAGERSTRTM, RICHARD
                                                            18.5%; Score 181.8; DB 3; 65.4%; Pred. No. 2.1e-41;
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                                        0; Mismatches 147;
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                                                                                                                                                  /product= "XLNA"
Q ID NO: 1:
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US-07-744-570B-1
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                                                                                                                                                                   APPLICATION NUMBER: US/07/744
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07744570B Patent No. 5202249
                                                            Matches
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNBER: US/07/744,570B
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shareck, F.
TITLE OF INVENTION: Xylanase for Biobleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kluepfel, APPLICANT: Morosoli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United ZIP: 94804-0023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Richmond
STATE: Californ
                                                                                                                                                          TOPOLOGY:
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127 ACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGT 186
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                                                          343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Box Number 4023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kluepfel, D.
Morosoli, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States
                                                          Conservative
                                                                                                                                                        Circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michael J. Bradley
                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 3.5 inch, 1.44Mb storage
                                                                        17.1%;
                                                        0;
                                                        Score 168.4; DB 2;
Pred. No. 1e-37;
0; Mismatches 211;
                                                          Indels 18;
                                                                                            Length 675;
                                                        Gaps
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RESULT 13
US-08-507-431-5
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                                                                                                                                                                                                                                                                                              TITLE OF
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                          COUNTRY: United States ZIP: 10174-6401
                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                        STREET: 405 Le
CITY: New York
                                                                                                                                                                                                                                            ADDRESSEE:
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5. 5693518
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                                                                                                                                                                                                                            405 Lexington Avenue,
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Si, Joan Q.
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Christgau, Stephan
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US-08-507-431-5
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US-08-902-655A-5
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Best Local Similarity
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APPLICATION NUMBER: US 60/002
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954
TELEPHONE: 212-870-0123
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
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                                                                        CGTGCAGA 737
                                                                                                        GGCTAAGA 710
                                                                                                                                                                 ATCGTTGCAACGGAGGGCTACTTCAGCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTG
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                                                                                                                                          ATCGTCGCTACTGAAGGCTACTACTCGTCTGGGTCTGCGTCCATTACGGTTGCCTGAGAG
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: AGY16, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERRENCE/DOCKET NUMBER: 39!
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
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ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
ADDRESSEE: No. 58858190 No. 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 30-July-1997
CLASSIFICATION: 435
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lir
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                      343
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                                                                                                                                                                                                                167 ATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCT
                                                                                                                                                                                                                                                                             107 CGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACT 166
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CTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTT 402
                                                    AGTGCTCATGACATTACGTACTCCGGCTCCTGGACCAGCACAGGAAATAGCAACAGCTAC
                                                                                                                                                                                GCTTCTGGACCGATGGCGCAAGCGGCGATGTTGAATACAGCAACGGCGCCGGGGGGGTCCT
                                                                                                                 ACAGCGTGACCTGGTCATCGGCCTCGAACTTCGTCGGTGGAAAGGGCTGGAACCCTGG-A
                                                                                                                                                                                                                                              CTGCCCTTGCTGGGCGCTCGACTGGCACTCCACTGGCTACTCGAACGGCTATTACTATA 193
                                                                                  TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC----AAACGGCAACAGCTAC 342
                                                                                                                                                   ACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCC 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mullertz, Anette
                                                                                                                                                                                                                                                                                                                  Conservative
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Munk, Niels
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Christgau, Stephan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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Dalboge, Henrik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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57.9%;
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ASPERGILLUS ACULEATUS
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Pred. No. 9.4e-37;
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US-09-116-622-5
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        TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION:
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                             REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 39:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60805670 No. 6080567disk of No. 6080567th America, STREET: 405 Lexington Avenue, 64th Floor CITY: New York
STATE: New York
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Agrie, Cheryl H.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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STRANDEDNESS:
                                                                                              TELEPHONE:
                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCATTTCAATGCCTGGGCGAAGCTGGGAATGAATCT---GGGCACGCACAACTATCAG
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Christgau, Stephan
Heldt-Hansen, Hans P.
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; LOCATION:
US-09-116-622-5
Search completed: February 11, 2006, 20:45:50 Job time : 216.809 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 AGTGCTCATGACATTACGTACTCCGGCTCCTGGACCAGCACAGGAAATAGCAACAGCTAC 372
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                                                           CCTGCAGA
                                                                                                                    ATCGTCGCTACTGAAGGCTACTACTCGTCTGGGTCTGCGTCCATTACGGTTGCCTGAGAG
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join(31..723, 727..849, 853..900, 904..927)
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Result
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DB seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration
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                                                                      US-10-213-990-65
US-10-213-990-68
US-09-770-621-1
US-09-770-621-1
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US-10-213-990-67
US-10-213-990-71
US-11-018-645-21
US-10-213-990-79
US-10-213-990-79
US-10-213-990-79
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US-10-425-115-177283
US-10-425-115-82922
US-10-425-115-37173
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7943.586 Million cell updates/sec
Sequence 65, Appl
Sequence 1, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 64, Appl
Sequence 67, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 31, Appl
Sequence 31, Appli
Sequence 1, Appli
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Sequence 9, Appli
Sequence 3, Appli
Sequence 177283,
Sequence 82922, A
Sequence 82927, A
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7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	8.0	8.0	8.2	8.4	8.4	8. 5	9.1	9.2	9.6	10.4	10.5
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US-10-237-386-10	US-10-626-724-12	US-10-626-724-6	US-10-626-583-12	US-10-626-583-6	US-09-909-207-11	US-09-909-207-10	US-09-909-207-5	US-09-909-207-4	US-09-909-207-2	US-09-909-207-1	US-11-018-645-10	US-11-018-645-3	US-10-437-963-15625	US-10-626-724-4	US-10-626-583-4	US-10-425-115-48309	US-11-018-645-19	US-11-018-645-15	US-11-018-645-13	US-10-340-860A-39	US-10-419-969-5
Sequence 10, Appl	Sequence 12, Appl	Sequence 6, Appli	Sequence 12, Appl	Sequence 6, Appli	Sequence 11, Appl	Sequence 10, Appl	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 3, Appli	Sequence 15625, A	Sequence 4, Appli	Sequence 4, Appli	Seguence 48309, A	Sequence 19, Appl	Sequence 15, Appl	Sequence 13, Appl	Sequence 39, Appl	Sequence 5, Appli

ALIGNMENTS

US-09-467-368-1

Sequence 1, Application US/09467368
Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette

Inge Helmer

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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
                        TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600
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TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
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CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
                                                                                                LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
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LOCATION: 31.70:
SEQUENCE DESCRIPTION:
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Best Local Simi:
Matches 983; (
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FEATURE:
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TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA
                                     GAGCCTGGCCAGGATCAGTAGTTGCTTTGCGGTGTTTTGCTCCCTATTCTCGTGAAAAAA
                                                 GAGCCTGGCCAGGATCAGTAGTTGCTTTTGCGGTGTTTTTGCTCCCTATTCTCGTGAAAAA
                                                                                    ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC
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Pred. No. 7.8e-305;
; Mismatches 0;
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APPLICANT: DATE: C. C. C. APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Jens
ITITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOPTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 588
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US-10-237-386-9
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; TYPE: DNA
; ORGANISM: Thermomyces
US-10-237-386-9
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Best Local Similarity
Matches 585; Conserv
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                CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTAC
                                                                                                                                    CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTAC
                                                                                                                  59.5%; Score 585; DB 6; Length 588; ilarity 100.0%; Pred. No. 5.7e-177; Conservative 0; Mismatches 0; Indels
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TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAA

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Sequence 3, Application US/09803454
Publication No. US20030022280A1
GENERAL INFORMATION:
APPLICANT: No. US20030022280A1ozymes A/S
APPLICANT: Takagi, Shinobu
APPLICANT: Takagi, Shinobu
APPLICANT: Terui, Yuri
ITILE OP INVENTION: High Expression of Industrial Enzymes
FILE REFERENCE: 6125.200-US
CURRENT APPLICATION NUMBER: US/09/803,454
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
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Matches
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LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
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CACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC 690
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                                                    GTTCANACTGGTTGTCATTTCGATGCTTGGGCTAGAGCTGGTTTGAATGTTAATGGTGAT
                                                                          GTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGAC
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US-10-425-115-177283
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APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 177283
LENGTH: 850
TYPE: NAN
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CCCACTTCGACGCCTGGGCCTCCAAGGGCATGCAGCT---CGGTCAGCACAACTACCAGA
                            GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
                                                                  TCAACCAGTACTGGTCCGTCCGCCAGAACAAGCGCAGCTCCGGCTCCAACATGAAGA
                                                                                                    TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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Pred. No. 1.6e-71;
0; Mismatches 228;
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TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTG

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Sequence 82922, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 82922

LENGTH: 749
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US-10-425-115-82922
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Best Local
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ORGANISM: Zea mays
FEATURE:
FEATURE:
LOCATION: (1)...(749)
OTHER INFORMATION: unsure a
FEATURE:
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al Similarity 63.9%;
423; Conservative
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Pred. No. 4e-68;
0; Mismatches 230;
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Sequence 37173, Application US/10425115

Sequence 37173, Application US/10425115

SEMERAL INFORMATION.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

ITITLE OF INVENTION: Nucleic Acid Molecules a
FILE REFERENCE: 38 c1 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 37173

LENGTH: 818
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US-10-425-115-37173
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Best Local Similarity
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ORGANISM: Zea mays
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CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC
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nilarity 62.5%;
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Pred. No. 4.1e-66;
0; Mismatches 241;
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APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OP INVENTION: NUCLEIC ACIDS OP ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT FILLING DATE: 2002-08-05
RUMBER OF SEO ID NOS: 72
SOPTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 65
LENGTH: 666
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(666)
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US-10-213-990-65
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; Publication No. L
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Best Local S
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                           GAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATC 507
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GAGAGCGACGGGGCCACGTACAACCTCTACAAGACGACGCGGACGAATGCGCCGTCCATC
                                                                                                                       AGCGGAAACGGCTACCTCTCCGTGTACGGCTGGACGACCAGTCCGCTGGTCGAATTCTAC
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llarity 61.5%;
Conservative
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Pred. No. 4.5e-61;
0; Mismatches 249;
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; LOCATION: (1)...(705)
US-10-213-990-68
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US-10-213-990-68
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TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10.182-019-999
CURRENT APPLICATION UNMERE: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 705
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Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
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Best Local Similarity
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ORGANISM: Aspergillus
FEATURE:
383
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                                                                                                              GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGC 373
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  TGATTGAGTACTACGTTGAGTCGTATGGTACATACAACCCCGGCAGCGGCGGTACCT 442
                             GCAGCTTCAACCCCAGCGGCAATGGCTACCTGGCTGTCTACGGCTGGACCACCAACCCCT
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ilarity 60.5%;
Conservative
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Pred. No. 1.5e-60;
0; Mismatches 250;
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RESULT 9
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              TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                    APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READAE
SEQUENCE CHARACTERISTICS:
                                   NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-JUL-1994
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 New Y
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release *1
                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
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1100 New York Ave., N.W. Suite 600
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Fagerstr m, Richard
Lantto, Raija
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           Sequence 1, Application US/10286993

Publication No. US20030148453A1

GENERAL INFORMATION:
APPLICANT: Mantyla, Arja

APPLICANT: Paloheimo, Marja

APPLICANT: Lantto, Raija

APPLICANT: Fagerstrom, Richard
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                                                                                                           US-10-286-993-1
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APPLICANT:

Lahtinen, Tarja

Palonerme, Lantto, Raija Lanttom, Richard

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US-09-770-621-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: No. US20010024815A1
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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GCGAGGGTGGCAACCCCGGCAACCCCGGG
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                                   CTGACGTGGCTAAGACGTAACCTGGTG
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Pred. No. 4e-52;
0; Mismatches 273;
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TITLE OF INVENTION: Production and Secretion of TITLE OF INVENTION: Fungi
FILE REFERENCE: 1716.034004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/120,804
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US/08/590,563
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR FILING DATE: 1996-01-26
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Best Local
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TYPE: DNA
ORGANISM: Actinomadura f.
FEATURE:
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SOFTWARE: PatentIn version 3.0
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LOCATION: (303)..(1337)
OTHER INFORMATION: Prod
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Similarity 58.6%;
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                           ACTACCAGATCATGGCGACCGAGGGCTACCAGAGCAGCGGTAGCTCCACCGTCTCCATCA
                                                              ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTG 694
                                                                                                                                                                                      CCCGGACCTTCCAGCAGTTCTGGAGCGTCCGGCAGCAGAAGCGGACCAGCGGCACCATCA
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US-10-213-990-67
; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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; ORGANISM: Aspergillus
US-10-213-990-67
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APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 739
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Best Local Similarity 57.8%;
Matches 412; Conservative
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GGCTGCCACTTCGACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGACCACTACTAC
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                                                                   ACCTTCACCCAGTACTGGTCTGTGCGCACCTCCAAGCGTACCGGCGCCACTGTCACCATG
                                                                                            ACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCCGGTACCGTCCAGACG
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Pred. No. 4e-50;
0; Mismatches 249;
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APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
ITITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
ITITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-99
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 712
LENGTH: 713
COGANISM: Aspergillus
ORGANISM: Aspergillus
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US-10-213-990-64
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Best Local Similarity 57.7%;
Matches 412; Conservative
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                                                                      CTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTT
                                                                                                            CTCCTATGACCCCTCCACGGGAGCCACCCATCTCGGCACCGTCGAGAGCGACGGGGCCAC
                                                                                                                                    CACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCAT
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TGACCAGTACTGGTCGGTTCGGACTTCGCACCGGCAGAGTGGAACTGTGACGACGAAGAA
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Pred. No. 4.1e-47;
0; Mismatches 253;
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RESULT 13

US-10-213-990-71

Sequence 71, Application US/10213990

Publication No. US20030082595A1

GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNTITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNTITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PASTSEQ for Windows Version 4.0
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71
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Best Local Similarity 59.3
Matches 340; Conservative
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TYPE: DNA
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                                       GGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGG
                                                                                      CATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACCGCGAATCACTTCAAGGCCTG
                                                                                                                                                                            GCACCAACAGGTCAACCAGCCTTCGATCGTCGGCACGGCCACCTTCAACCAATACTGGTC
                                                                                                                                                                                                                                                                     CTCGGGCATGACGCACAAGGGCACCGTCACCAGCGATGGATCCACCTACGACATCTATGA
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GGCTAGTCTGGGGATGAA--
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Pred. No. 5.6e-42;
O; Mismatches 221;
  - CCTGGGTACCCATAACTATCAGATTGTTTCCACTGAGGG
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Sequence 21, Application US/11018645
Publication No. US20050208178A1
GENERAL INFORMATION:
APPLICANT: Bauer, Michael
APPLICANT: Bedford, Michael
APPLICANT: Bedford, Michael
APPLICANT: Bulliam, Derrick
TITLE OF INVENTION: Microbially Expressed Xy.
TITLE OF INVENTION: Uses
FILLE RETERERUES: 70357WOPCT
CURRENT APPLICATION NUMBER: US/11/018,645
CURRENT FILING DATE: 2004-12-20
CURRENT FILING DATE: 2004-12-20
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, LOCATION: (1)..(978)
US-11-018-645-21
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US-11-018-645-21
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SEQ ID NO 21
LENGTH: 978
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Best Local Similarity
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PRIOR FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 39
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OTHER INFORMATION:
FEATURE:
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                     GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
                                                             TCGAAGCGCGTGGGCGCACCATCACCATCGCCAACCATTTCAACGCCTGGGCCACGCTG
                                                                                                                                                               ACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGC
                                                                                                                                                                                                                                                                                                      GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC
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GGCATGAA---CCTGGGCCAGCACAACTACCAGGTCATGGCCACCGAGGGTTACCAGAGC
                                                                                               GACAAGCGCACCAGCGGTACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCT
                                                                                                                                   GTGAACCAGCCATCCATCATCGCCAACGCCACGTTCTACCAGTACTGGAGCGTGCGGCAG
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ilarity 56.8%;
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APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70
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; ORGANISM: Aspergillus
US-10-213-990-70
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APPLICANT: Jiang, Bo
APPLICANT: Bussey, I
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Best Local Similarity
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Storms, Reg
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                                                                                                                                                                          ACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCG 592
                                                                                                                                                                                                                                              TCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAAT
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CTGAGGGATATGAGAGCAGCGGTACCTCGACCATCACTGT
                                CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                    AGGCCTGGGCTAGTCTGGGGATGAA---CCTGGGTACCCATAACTATCAGATTGTTTCCA
                                                                                                 ACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA
                                                                                                                                       ACTGGTCCATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACCGCGAATCACTTCA
                                                                                                                                                                                                            TCTATGAGCACCAACAGGTCAACCAGCCTTCGATCGTCGGCACGGCCACCTTCAACCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10213990 No. US20030082595A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 4.1e-36;
0; Mismatches 148;
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Search completed: February 11, 2006, 23:51:27 Job time: 1025.32 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbm (Published_Applications_AA_New).

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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5: /cgn2 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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US-11-108-163B-1
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Sequence 191, App
Sequence 193, App
Sequence 213, App
Sequence 215, App
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. 4 14.9 1047 7 . 8 14.4 1077 7 . 2 13.3 1047 7 . 8 13.0 1029 7 . 8 13.0 747 7 . 8 12.6 669 7 . 11.8 10.66 7 . 11.8 10.66 7 . 11.9 10.68 7 . 10.9 633 7 . 10.9 635 7 . 10.9 636 7 . 10.9 636 7 . 10.9 636 7 . 10.9 636 7 . 10.9 10.8 570 7 . 10.9 10.8 570 7 . 10.9 10.9 10.9 10.9 10.9 10.9 10.9 10.	45	44	4	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22
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	9.1	9.2	9.3	9.3	9.3	9.3	9.4	9.5					11.0	11.1	11.7	11.8	12.0						14.4	14.9
7 US-10-517-939-181 7 US-10-517-939-181 7 US-10-517-939-161 7 US-10-517-939-227 9 US-10-517-939-317 1 US-10-517-939-317 1 US-10-517-939-167 1 US-10-517-939-17 1 US-10-517-939-153 9 US-10-517-939-153 1 US-10-517-939-153 1 US-10-517-939-251 1 US-10-517-939-353 1 US-10-517-939-163 1 US-10-517-939-163 1 US-10-517-939-163 1 US-10-517-939-173 1 US-10-517-939-173	1077	570	1053	645	678	570	1338	1068	570	1983	555	636	633	1020	1068	1086	669	642	1695	747	1029	1047	1077	1047
US-10-517-939-161 US-10-517-939-161 US-10-517-939-161 US-10-517-939-219 US-10-517-939-217 US-10-517-939-217 US-10-517-939-211 US-10-517-939-211 US-10-517-939-205 US-10-517-939-207 US-10-517-939-163 US-10-517-939-353 US-10-517-939-367 US-10-517-939-367 US-10-517-939-367 US-10-517-939-367 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-377 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	11	7	7	7	7	7	7
	US-10-517-939-369	US-10-517-939-375	US-10-517-939-191	US-10-517-939-157	US-10-517-939-171	US-10-517-939-377	US-10-517-939-367	US-10-517-939-163	US-10-517-939-189	US-10-517-939-353	US-10-517-939-251	US-10-517-939-197	US-10-517-939-207	US-10-517-939-153	US-10-517-939-205	US-10-517-939-211	US-10-517-939-167	US-11-214-413-31	US-10-517-939-317	US-10-517-939-227	US-10-517-939-219	US-10-517-939-161	US-10-517-939-181	US-10-517-939-299
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181, App 161, App 161, App 227, App 317, App 317, App 231, App 231, App 231, App 231, App 231, App 251, App 251, App 251, App 251, App 251, App 367, App 369, App	App	₽pp	App	App	App	Ąpç	App	App	App	App	App	Apr	App	Apr	App	App	App	App	ĄgĄ	App	App	App	App	ddw

ALIGNMENTS

RESULT 1 US-11-170-653-9

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CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITIE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 585; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                   124 CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC 183
                                                                                                                   184 GGTGGAGGGCAGGCCACGTACACCCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA 243
                                                                                             64
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                           GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATC 303
                                                                                                                                                                                     CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC 63
GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATC
                                                                                             GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA
                                                                                                                                                                                                                                                                              59.5%; Score 585; DB 11; ilarity 100.0%; Pred. No. 1.9e-148; Conservative 0; Mismatches 0;
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US-10-517-939-231
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APPLICANT: Esteghhalian, Alireza
APPLICANT: Esteghhalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS EN
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: DATE: 2003-06-16
                                                                                                                                                                                      Query Match
Best Local S
Matches 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steer, Brian
APPLICANT: Callen, Walte
APPLICANT: Healey, Shauu
APPLICANT: Hazlewood, Ge
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian,
                                                                                                                                                                                                                                                    SOPTWARE: FASTSEQ for Windows Version
SEQ ID NO 231
LENGTH: 1008
TYPE: DNA
ORGANISM: Bacteria
S-10-517-939-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 231, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
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193
                                                           133 GTCACGACCAACCAGGAGGGCACCAACAACGGCTACTACTACTCGTTCTGGACCGACAGC
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                                                                                                                                                                                        386;
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                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACC
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CAGGGCACCGTCTCCATGAACATGGGCTCCGGCGGTCAGTACAGCACCTCGTGGCGCAAC
                        GGAGCGCAGGCCACGTACCACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGAT
                                                                                                                           GTCGCGCTGGCGCGCTCGCCGCGCGCGATGCTGCCGGGCACCGCCCAGGCCGACACGGTC
                                                                                                                                                         GCCGCGACTGGGCCCTGGCCTTCCCCGGCAGGAATGCCACGGAGCTCGAAAAGCGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Callen, Walter
Healey, Shaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hazlewood, Geoff
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5. US20060003433A1
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                    20.6%;
                                                                                                                                                                                      Score 202.2; DB 7;
Pred. No. 5.7e-45;
0; Mismatches 258;
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                                                                                                                                                                                                                    Length 1008;
                                                                                                                                                                                          Indels
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                             246
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252
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Sequence 1, Application US/11108163B
Publication No. US20060014247A1
GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Kallio, Jarno
APPLICANT: Kallio, Jarno
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                                                                                                                                           ; OTHER INFORMATION: Nf xynllh nucleotide sequence (AJ508952), the coding region ; OTHER INFORMATION: from nt 303 to nt 1337 US-11-108-163B-1
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                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR PILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1275
                                                                         Matches
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                    TYPE: DNA ORGANISM: Nonomuraea flexuosa FEATURE:
                                                                                                                                                                                                                                                              LENGTH: 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      667
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 349
                                                                         403;
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Kallio, Jarno
Puranen, Terhi
Lantto, Raij
Suominen, Pirkko
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   TCGGCCTCCGGCGCATCGTCACCAGTGCCTTCGCCCTGGCACTCGCCATCGCCGGTGCGC
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                                                                       Score 197.2; DB 11; Length 1375; Pred. No. 1.4e-43; 0; Mismatches 273; Indels 12;
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Sequence 5, Application US/11108163B
Publication No. US20060014247A1
GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
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                                            APPLICANT: Suomine, Pirkko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE REPERENCE: 1716.034000B/MAC/DDN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2005-04-18
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 5
LENGTH: 663
TYPE: DNA
OCCANITAL NUMBER: US 60/562,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -11-108-163B-5
                                                                                                                                                                                                                                                                                                    APPLICANT:
                  ORGANISM: Nonomuraea flexuosa FEATURE:
OTHER INFORMATION: am24*, like am24 but 9 codons are changed in the sequence like
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Pagerstrom, Richard
Kallio, Jarno
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Lantto, Raij
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RESULT 5
US-11-108-163B-4
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APPLICANT: Suominen, pirkko

APPLICANT: Suominen, pirkko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR FILING DATE: 2005-04-18

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.3

SEQ ID NO 4

LENGTH: 906

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/11108163B Publication No. US20060014247A1
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Best Local
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APPLICANT: Mantyla, Arja
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Lantto, Raij
                                                                                                                                                                                                                                                                                                                         Fagerstrom, Richard
Kallio, Jarno
                                                                                                                                                                                                                                                                                                                                                                     Leskinen, Sanna
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Pred. No. 8.6e-42;
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APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richa
APPLICANT: Kallio, Jarno
APPLICANT: Puranen, Terhi
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           Sequence 3, Application US/11108163B Publication No. US20060014247A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR PILING DATE: 2004-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: am35*, like am35 but 9 codons are changed in the OTHER INFORMATION: Example 10 (the changes do not alter the encoded OTHER INFORMATION: sequence)
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Leskinen, Sanna
Fagerstrom, Richard
Kallio, Jarno
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Pred. No. 9.6e-42;
0; Mismatches 218
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                                                                                                                                                      APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Rich
APPLICANT: Kallio, Jarno
                     APPLICANT: Suominen, Pirko TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi FILE REFERENCE: 1716.034000B/MAC/DJN CURRENT APPLICATION NUMBER: US/11/108,163B CURRENT FILING DATE: 2005-04-18
                                                                                                                          APPLICANT:
                                                                                                                                        APPLICANT:
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APPLICATION NUMBER: US

INFORMATION:

Fagerstrom, Richard Kallio, Jarno Puranen, Terhi Lantto, Raij

Level Ö.

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; TYPE: DNA
; ORGANISM: NONOMURAEA f
; FEATURE:
; OTHER INFORMATION: am2
US-11-108-163B-3
RESULT 7
US-11-108-163B-2
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Best Local 9
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Pred. No. 6.3e-41;
0; Mismatches 220;
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Sequence 225, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healewood, Geoff
APPLICANT: Mu, Di
APPLICANT: Blum, David
APPLICANT: Buteghlalian, Alireza
TITLE OF INVENTION: XYLAWASES, NUCLEIC ACIDS ENCODING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 906
TYPE: DNA
ORGANISM: Nonomuraea flexuosa
FEATURE:
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Local Similarity 60.9%;
nes 361; Conservative
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Pred. No. 7e-41;
0; Mismatches 2
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                                        Sequence 165, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
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US-10-517-939-165
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SEQ ID NO 225
LENGTH: 1059
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Matches 346; Conserva
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                             APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
    APPLICANT:
TITLE OF I
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T: Wu, Di
T: Blum, David
T: Esteghlalian, Alireza
INVENTION: XYLANASES, NU
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    NUCLEIC
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265 TCGGGCTCGTTCAACTCACCCGGCAATGGTTATCTCACCCTGTACGGTTGGACCACCAAT
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Pred. No. 1.2e-40;
D; Mismatches 223;
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FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER: 60/380
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 165
LENGTH: 1047
                                                                           RESULT 10
US-10-517-939-199
; Sequence 199, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
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Best Local :
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoi
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                                                                                                                                                                                           ATCACGGTGAGCGATGGCGGC
                                                                                                                                                                                                                      ATCACCGTTGCTGACGTGGGC
                                                                                                                                                                                                                                                                                      GGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGC
                                                                                                                                                                                                                                                                                                                      GGAACCATCTCCACCGGCAACCATTTCGACGGCTGGGCGACGTTCGGCATGAA---CCTG
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Pred. No. 2.6e-40;
0; Mismatches 215;
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
ITITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENG
ITITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT FILING DATE: 2004-12-13
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: FCT/US03/19153
PRIOR APPLICATION NUMBER: FCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 199
LENGTH: 1074
TYDE: DNA
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Best Local !
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                               CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                                                                                                 ACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCG
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 cceaesecraccaeaecaececaecreceacarcaceer
                                                                 ATGCCTGGGCCAGCCTCGGCATGAA----CCTGGGACAGCACAACTACCAGGTGATGGCCA
                                                                                                 <u>ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA</u>
                                                                                                                                   <u>ACTGGAGCGTGCGGCAGTCGAAGCGCACCGGCGGCACCATCACCACGGCCAACCACTTCA</u>
                                                                                                                                                                                                     TCTATCGCACGCAACGGGTCAACCAGCCGTCGATCATCGGCACCGCGACGTTCTACCAGT
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Pred. No. 2.9e-36;
0; Mismatches 260
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AND USING
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APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Blum, David
APPLICANT: Esteghialian, Alireza
APPLICANT: Esteghialian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEI
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEI
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: FOT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 50/389,299
PRIOR APPLICATION NUMBER: 50/389,2
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; OTHER INFORMATION:
US-10-517-939-255
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APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geof
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
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CGGAGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
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                                                                  ATGCCTGGGCCAGCCTCGGCATGAA----CCTGGGACAGCACCAACTACCAGGTGATGGCCA
                                                                                                                                  ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA 652
                                                                                                                                                                                                     ACTIGGAGCGTGCGGCAGTCGAAGCGCACCGGCGCGCACCATCACCACGGCCAACCACTTCA 625
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57.5%;
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Pred. No. 3e-36;
0; Mismatches 2
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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
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US-10-517-939-169
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Best Local Similarity
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APPLICANT: Callen, Wall
APPLICANT: Healey, Shar
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APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING
FILE REFERENCE: 564462007901
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TYPE: DNA
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ACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTAC
                                                                                                                                                                                                                                                                                         AGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGGTGGTCGAGTATTACATCGTCGAG 396
                                                                                                                                                                                                                                                                                                                                                     AACCCCGGCCTGAACGCCAAGAGACCCATTTGAGGGTGTTTACCAGCCAAACGGCAAC 336
                                                                                                                                                                                                                                                                                                                                                                                                GGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGG 276
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                                                     GCCACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGAAGCGCGTCGGCGGCACGATCACC
                                                                                 CAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAG
                                                                                                                                                    GGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACC
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                                                                                                                      GGCGGCACCTATGACATCTACCGCACGCAGCGCGTGAACCAGCCTTCCATCATCGGCACC
                                                                                                                                                                                          AGCTGGGGCACCTATCGACCGCCGGGCGGCCAGGGCTTCATGGGCACCGTCAACAGCGAT
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Healey, Shaun
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Pred. No. 3.9e-35;
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APPLICANT: Bateghlalian, Alireza
ITITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
ITITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
ITITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
ITITLE REFERENCE: 564462007901
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: FCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 1044
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US-10-517-939-221
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APPLICANT: Callen, Waltu
APPLICANT: Healey, Shau
APPLICANT: Hazlewood, G
APPLICANT: Wu, Di
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                                                                                                                                                                                                                     GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTTCTACGGTTGGACCCCGCAACCCGC
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                    ATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCA
                                                                                                                             CGTTCAACTCGCC---
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ACCAGCCTTCCATCATCGCCACCGCGACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGA
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Healey, Shaun
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Pred. No. 4.5e
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR PPLICATION NUMBER: 60/389,299
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEO ID NOS: 380
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Best Local (
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APPLICANT: Caller
APPLICANT: Healer
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TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
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APPLICANT:
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FEATURE:
OTHER INFORMATION: Obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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mes 351; Conserv
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                                                                                                                                                                                                                                                                                        130 ACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 189
                                                                                                310 GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC
                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                 TGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCG 673
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                    GGTAACCTCGTCGGTGGAAAGGGCTTGAACCCCGGCCTGAACGCAAGAGCCATCCACTTT
                                                                                                                                                                                                AACGCCACCATGACACTCGGTGCCGGTGGAAACTATTCTTCATCCTGGAACAGCACCACT
                                                                                                                                                                                                                              GCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGC
                                                                 TCGGGCAGTTATAGCGCGAGTGGAACCAGCTACCTCGCACTTTACGGCTGGACTCGAAAC
                                                                                                                                 AACAACTGGGTTGGCGGTAAAGGCTGGATGCCGGG---TACTCGGCGCACAGTCACCTAT
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CCGCTGATCGAATATTACATTGTCGAAAACTGGGTCAATTACAATCCTGCGTCCGGCGCA
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Wu, Di
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Healey, Shaun
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o. US20060003433A1
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                                                                                                                                                                                                                                                                                                                                                                                                Score 165.4; DB 7;
Pred. No. 5.5e-35;
0; Mismatches 266;
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   384
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APPLICANT: BUM, DAVID
APPLICANT: ESteghlalian, Alireza
INTILE OF INVENTION: XYLANASES, NUCLEIC ACIDS EN
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REPERENCE: 564462007901
CURRENT PILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: CT/US03/19153
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2003-06-14
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 217
LENGTH: 1083
TYPE: DNA
ROANISM: Unknown
FEATURE:
PRIOR TIMPORMATTON: Obtained from an environme
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APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Geoff
APPLICANT: Hy, Di
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US-10-517-939-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-517-939-217
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 359; Conserv
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                                                                                                    AACAACTGGGTCGGCGAAGGGCTGGTCGACCGGCTCCAGC---CGCACCGTCAGCTAT
                                                                                                                        GGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTT
                                                                                                                                                                                                                                                                          ACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 189
TCGGGCAGCTTCAATTCGCCCGGCAACGGCTACCTGACTCTACGGGTGGACCACCAAC
                                                                                                                                                                     GGCACGGTGAACTTCTGCATGTACCCGAATGGCCGCTACACCTCGAACTGGAGCGGCATC
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o. US20060003433A1
                                                                                                                                                                                                                                                                                                          16.4%;
ilarity 56.8%;
Conservative
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                                            TCTCGCGAGGCAACAGCCAAGAATGTCGTCAG
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Search completed: February 11, 2006, 22:06:15
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10984.434 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd
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U35436 Thermonyces
BX842624 Neurospor
U24191 Trichoderma
X76047 H.insolens
165436 Sequence 3
BD006885 Appergill
AY159910 Trichoder
AF246830 Fusarium
AJ012718 Trichoder
AF46830 Fusarium
AJ012718 Trichoder
AK110604 Oryza sat
AY648860 Gibberell
AY536639 Aspergill
B28868 Xylanase ge
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Matches 675; Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
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Submitted (06-SEP-1995) Institute of Biotechnology,
Biocatalysis, TU-Graz, Petersgasse 12,, Graz 8010,
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Thermomyces lanuginosus
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ITVADVG"
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Pred. No. 5.6e-106;
); Mismatches 0;
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65227736 /denc="B10D6.040"	gene	HAMPE AS ENVISOR LABELY BY AND ASSESSED TO A SECOND FOR A SECOND ASSESSED TO A	
/gene="B10D6.030" /number=2	excii	WIESPS'IV PETUTIO IS THE TOTAL THE TOTAL THE TOTAL THE TOTAL TO THE TOTAL TH	
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/gene="B1006.020" /number=2		E-mail: ulrich-schulte@uni-duesseldorf.de BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic	COMMENT
complement (35093850)	exon	G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,	
=		Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:	
<pre>/number=1 complement(30333508)</pre>	intron	Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH.	JOURNAL
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DIYSPOLVELSKKLERFILIDDLVEFTPERAPLILEHVILITRITVIKIKIRKÆKÆKK DIYSPOLVELSKKLERFILIDDLVEFTPERAPLILEHVILITRITVIKIKIRKÆKÆKK		Schulte, U., Aign, V., Honesei, J., Brandt, F., Fartmann, B., Holland, R., Nyakatura, G., Mewes, H.W. and Mannhaupt, G.	AUTHORS
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.3850,3914.	gene	group I BAC clone B10D	DEFINITION
	gene	89019	
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GTGGAGTGACGGTGGAGGCCAGGCCACGTACACCAACCTGGAAGGCCGCCACCTACGAGAT
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                                                                                          CGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTG 143
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AQNCQPKVVRVPERPTSGIKYVKLDNCHMYKLKYASKARQLNGQQHVEAVDSSNAPVI
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/gene="B10D6.040"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="CAE76222.1"
/db_xref="GI:38566919"
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12129 ..12141,12579 ..12829,13172 ..13577,13679 ..14071,
14173 ..14195,14433 ..14924,14995 ..15128,15186 ..15281,
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/gene="B10D6.040"
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/gene="B10D6.050"
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/gene="B10D6.050"
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Submitted (06-APR-1995) Willem H. van Zyl, University of
Stellenbosch, Microbiology, Victoria street, Stellenbosch, 7600,
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Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.
U24191
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1a Grange, D.C., Pretorius, T.S. and van Zyl, W.H.
Expression of a Trichoderma reesei beta-xylanase
Saccharomyces cerevisiae
Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996
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Hypocrea jecorina
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Hypocreaceae, Hypocrea.
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105. .776
/codon_start=1
/product="beta-xylanase precursor"
/protein_id="AAB50278.1"
/db_xref="GI:780816"
                                                                                                                     /note="endo-beta-1,4-xylanase; endoxylanase"
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GYFHSYWNDGHGGVTYTNGPGGQPSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPN
GNSYLSVYGWSRNPLIEYYIVGNFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPS
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/product="beta-xylanase"
and Hansen, H.P.H.
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'mol_type="mRNA"
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/db_xref="GI:505261"
/db_xref="GOA:P55334"
/db_xref="GOA:P55334"
/db_xref="InterPro:IPR001137"
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PSIDGTRTFQQYWSIRKNKRVGGSVNMQNHFNAWQQHGMPLGQHYYQVVATEGYQSSG
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Be Ka, R.Michael, Yoder, W., Takagi, S. Aspergillus expression system Patent: US 5667990-A 3 16-SEP-1997; Location/Qualifiers
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165436
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                                                                                                              CTATACCGACGGCGATCAGTATGACATCTTTGTGAGCACCCGCTACAACCAGCCCAGCAT
                                                                                                                                                            TGTCATCGAGTCGTACGGCACGTACAATCCCCGGCAGGCTCAGTACAAGGGCACATT
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                     CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCACGGAATGCCGCT---CGG
                                                                                                                                                                               CATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGT
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TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT 656
                                          CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
                                                                                                                                    CGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCAT
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/mol_type="unassigned
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Pred. No. 1.8e-39;
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Aspergillus expression system
Patent: JP 2001025393-A 2 30-JAN-2001;
NOVO NORDISK BIOTECH INC
OS Humicola insolens
PN JP 2001025393-A/2
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Berka,R.M., Yoder,W., Takagi,S. and Boominazan,C.
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TGTCATCGAGTCGTACGGCACGTACAATCCCCGGCAGCCAGGCTCAGTACAAGGGCACATT
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RANDY M BERKA, WENDY YODER, SHINOBU TAKAGI,

CARAPPAN CHETYER BOOMINAZAN

C12N15/09,C12N1/15,C12P21/02//(C12N15/09,C12R1:66),(C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N15/09,C12N
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/mol_type="genomic DNA"
/db_xref="taxon:34413"
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Pred. No. 1.8e-39;
0; Mismatches 210
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Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
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Min,S.Y., Kim,B.G. and Ahn,J.-H.
Purification, Characterization,
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Min,S.Y., Kim,B.G. and Ahn,J.-H.
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Trichoderma viride scomplete cds.
AY320048
                                                                                                        Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology
Fermentation Technology of Yunnan, School of Life Science, Yunnan
University, 2 North Road, Green Lake, Kunming, Yunnan 650091, Chir
Location/Qualifiers
                                                                                                                                                                                                            Cloning and characterization Trichoderma viride YNUCC0183 Unpublished 2 (bases 1 to 672)
                                                                                                                                                                                                                                                               Li, W.P., Zhang, Q., Yang, Z.W.
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Tricoderma viride species complex.
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Trichoderma viride
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Direct Submission
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W.P., Zhang,
                          /organism="Trichoderma v
/mol type="mRNA"
/strain="YNUCCO183"
/db_xref="taxon:5547"
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/EC_number="3.
/codon_start=1
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               number="3.2.1.8"
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AF246830
       Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 2202)
                                                      Fusarium oxysporum f. sp. lycopersici
Fusarium oxysporum f. sp. lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                            AF246830
Fusarium oxysporum
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GYYYSYMNDGHSGVTYTNGAGGSFSVNWANSGNFVGGKGWNPGSSSRVINFSGSYNPN
GNSYLSVYGWSKNPLIEYYIUENFGTYNPSTGTTKLGEVTSDGSVYDIYRTQRVNQPS
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/protein_id="AAP83925.1"
/db_xref="GI;32481057"
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Submitted (17-MAR-2000) Departamento (Cordoba, Avda. San Alberto Magno s/n,
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                  /translation="MVHFTSVFAGLSLVAGSLAAPSKEGLFSKITKRAGTPNSSGTNN GFYYSWMSDGCADATYTNGEGGSYSMEWKDGGNVVGGKGWSPGKARTISYEGEYKENG NSYLSVYGWTRNFLVEYYIVESFGTYNPSGGATKKGTVEADGSTYDIFETTRTNAPSI DGTQTFQQYWSVRQDKSTGSVDTGLHFDAWEKAGMKLGTHDYQILATEGYFSSGSSH MTVSEGASSGGAGGSTGGDASQGGDSQQGGDVQQGGDASQGGNGQQGGNGNSFQQPG
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/product="xylanase 5 protein"
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/db_xref="GI:13491873"
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/note="forma_specialis:
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Trichoderma viride
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Mutations in the Active Site of the Ethylene Inducing
Elicitor Inhibits the b-1-4-Endoxylanase Activity But
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CTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGG
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                                                                                                          CGTGGACGTGGAGAGCGCCAGACGATTGGCCCCGGCACTGGCTTCAACAACGGCTACTA
                                                                                                                                        CACGGAGCTCGAAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTA 134
                                                                                                                                                                      CCTCGCAGGCTTCGTCGCTGTTACCGGAGTTCTGTCCGCTCCCACTGAGACCGTGGAGGT 142
                                                                                                                                                                                                  CCCCGTTGCCCTTGCCGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGGCAGGGAATGC
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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endo-1,4-beta-xylanase.
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KEYWORDS
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                                                                                                                                                                                                                                                              TTACCAGTACTGGTCTGTCCGCCGCAACCA-CGCTCCAGCGGCTCGGTCACGGTTGCGAA
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                                                                                                                           CCACTTCCAACGCGTGGCGAACCTGGGCTTGA--CTCTGGGAACCTTGGACTACCAGAT
                                                                                                                                                                                         CCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGAT
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Oryza sativa (japonica cultivar-group) sequence 912 ģ mRNA cDNA clone:002-168-G08, linear PLN 24-JUL-2003

AKI10604.1 GI:32995813

PLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
M Oryza sativa (japonica cultivar-group)
Eukaryota; viridiplantae; Streptophyta; Embr Spermatophyta; Magnoliophyta; Liliopsida; Po Ehrhartoideae; Oryzeae; Oryza. Embryophyta; Track a; Poales; Poaceae; Tracheophyta;

Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J. The Rice Full-Length cDNA Consortium, National Institute of

Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Karosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Miikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, K., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice Science 301 (5631), 3 12869764 2 (bases 1 to 912)

376-379 (2003)

2 (bases 1 to 912)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Adachi, J., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hira Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hramoto, K., Hira Hori, F., Hotta, I., Iida, J., Iida, Y., Ishikawa, M., Itoh, M., Kanarashi, K., Ishibiki, J., Ishihi, Y., Ishikawa, M., Itoh, M., Kanarashi, K., Ishibiki, J., Ishibira, N., Kanarashi, K., Ishibikawa, K., Ishibika, J., Ishibikawa, M., Itoh, M., Kanarashi, K., Ishibikawa, K., Ishibikawa, K., Ishibika, J., Ishibikawa, K., Ishibikawa, K., Ishibikawa, K., Ishibika, J., Ishibikawa, K., Ishibikawa, K., Ishibikawa, K., Ishibika, J., Ishibikawa, K., Ishibika Kawagashira, N., Hiraoka, T., Kagawa, I. Doi, K.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibate, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akshira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head Laboratory of Gene Expression; 2-1-2 Kamnondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto, M.
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                    CTCGAAAAGCGACAGACACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCC 141
GTGCAGTGGCGCAACACTGGCCAACTTCGTCGGTGGGAAGGGGATGGAACCCAGG---AACC
                                      ATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAAC 261
                                                                                        TGGTGGACCGATGGCGGCGCTCTGCCATATACACCATGGGCGAGGGCTCCAAGTACACT 278
                                                                                                                                           TGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAG 201
                                                                                                                                                                                      CTTGAGAGGCGCCAGTCCACCGCCAACTCAGTCGGAACTCACAACGGCTACTTTACTCG
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/db_xref="taxon:39947"
/clone="002-168-G08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                              31.6%;
                                                                                                                                                                                                                                                                                       Score 213; DB 15;
Pred. No. 4.6e-34;
0; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                                  Length 912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 696)
Hatsch,D., Phalip,V. and Jeltsch,J.-M.
The xylanases of Gibberella zeae
uppublished
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Gibberella zeae
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Hatsch,D., Phalip,V. and Jeltsch,J.-M.
Direct Submission
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xylanase
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Submitted (09-JUN-2004) Laboratoire de Phytopathologie, IFR 85 - ESBS -UIP, Boulevard Sebastien Brant - BP10413, Illkirch-Graffenstaden, Alsace 67412, France Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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614 TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
                                                                                                                                                                                                                           398 GTTCTTACAACCCCGGCAGCCAGGCTCAGCACGAGGTACCGTCTACACCGACGGTGACA
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                                                      ACCACTTCAATGCTTGGAGATCTGCTGGCATGAA---CCTCGGAAACCACTACTACCAGA
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                                                                                                                                                                       GCACCTATGATCCTTCCGGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 433
                                                                                                                                                                                                                                                                                    TTTGCGTTTACGGATGGACCCGCGGTCCCCTCGTCGAGTACTACGTCATCGAGAGTTACG 397
                                                                                                                                                                                                                                                                                                         TTGCGGTCTACGGTTGGACCCGGAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTG 373
                                                                                                                                                                                                                                                                                                                                            G---TACTGGCCGAACCATCAACTACGGAGGTTCCTTCAACCCTCAGGGTAACGGATACC
                                                                                                                                                                                                                                                                                                                                                                       GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACC 313
                                                                                                                                                                                                                                                                                                                                                                                               ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTCGGTAGAAAGGGATGGAACCCTG
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                                                                                                               TCAACCAGTACTGGTCCATCCGCCGCAACAAGCGTACCAGCGGCTCCGTCAACATGCAGA 577
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Search completed: February 11, 2006, 20:54:07 Job time : 3495.06 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
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Gapop 10.0 , Gapext 1.0
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675
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 2 3 3 4 4 1 1 1 1 1 1 1 1 1 1 1 1	Score 675 675 5875 371.6 239 221.6 221.6 203.4 203.4	Query Match 100.0 100.0 100.0 100.0 35.4 35.4 35.4 35.4 30.1 30.1	Query Match Length Match Length 983 100.0 983 100.0 983 55.1 678 55.1 678 35.4 1123 35.4 1123 35.4 1123 35.4 1125 30.4 1195 30.4 1195 30.4 1195 30.4 1195 30.1 576 30.1 576 30.1 696 29.8 1085) 1 1 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2	
- ?	675	100.0	983	2 6	AAT4074
N	675	100.0	983	N	AAT43010
w	582	86.2	588	_υ	AAS13813
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6	221.6	32.8	705	10	ABQ80364
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18	190	28.1	1015	N	AA054775
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150.2	150.6	150.8	153.6	156.2	159	159.8	160.8	160.8	164	164.6	165.4	165.4	165.6	165.8	168.4	170	170	171.8	181.2	181.8	183.4	185	186.2	187.8	147.1
22.3	22.3	22.3	22.8	23.1	23.6	23.7	23.8	23.8	24.3	24.4	24.5	24.5	24.5	24.6	24.9	25.2	N	N	2	2	Ŋ	27.4	27.6	27.8	1
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12	12	12	12	12	N	12	12			N	12	10	12	12	N					N	N	12	12	N	į
ADJ34943	ADJ35017	ADJ34999	ADL23220	ADJ35037	AAQ69150	ADJ35001	ADJ34967	ADJ34979	AAQ28828	AAQ74638	ADJ34961	ABQ80366	ADJ35005	ADJ34953	AAQ36563	ADJ35039	ADJ34983	AAQ43458	ABQ80361	AAT71585	AAQ03405	ADJ34949	ADJ35009	AAQ90388	
Adj34943 DNA	_	DNA	Adl23220 A. niger	7 DN	Aaq69150 Aspergill	Adj35001 DNA encod	Adj34967 DNA encod	Adj34979 DNA encod	Aaq28828 Recombi	Aaq74638 Aspergill	Adj34961 DNA encod	Abq80366 A. fumiga	Adj35005 DNA encod	Adj34953 DNA encod	Aaq36563 Endo-xy	Adj35039 DNA encod	Adj34983 DNA encod	Aaq43458 Sequence	Abq80361 A. fumiga		Aaq03405 Streptomy	Adj34949 DNA encod	Adj35009 DNA encod	Aaq90388 Xylanase	

ALIGNMENTS

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RESULT 1
AAT40742
ID AAT4
XX AAT4
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Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssochlamus; Paecilomyces; animal feed additive; in-vivo breakdown; plant cell wall; growth rate; feed conversion; ss.

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26-JAN-1995;
                                                  01-AUG-1996.
                          26-JAN-1996;
                                                                          W09623062-A1.
 95DK-00000094
                          96WO-DK000046
                                                                                                                           31. .708
                                                                                                 /*tag= a
/product= "xylanase"
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Hansen PK, Wagner P, Muellertz A, Knap IH;

(NOVO) NOVO-NORDISK AS

WPI; 1996-454790/45. P-PSDB; AAW01112.

Fungal xylanase prepns. for use as animal feed additives -construct for producing recombinant Thermomyces xylanase. and DNA

Claim 5; Page 45-46; 69pp; English.

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RESULT 2
AAT43010
ID AAT4
XX
AC AAT4
XX
DT 16-0
DT 22-F
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
16-OCT-2003
22-FEB-1997
                                          AAT43010;
                                                                     AAT43010
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                                                                     standard;
                                                                                                                                                         GTTGCTGACGTGGGC 675
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                                                                                                                                                                                                                                                                           GTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGAC
                                                                                                                                                                                                                                                                                                                                        GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACC
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(first entry)
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Pred. No. 2.6e-174;
Mismatches 0;
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Matches 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bread improving additive contg. xylanase from Thermomyces - and alpha-amylase, increases volume, improves anti-staling propertie
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Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endo-1,4-beta-D-xylanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jorgensen OB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-1996;
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                                                                                                                                                                                                                                            Sequence
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                                                                                               | CCGGCAGGGAATGCCACGGAGCTCGAAAAAGCGACAGACCCCCCAACTCGGAGGGCTGG
                                                                                                                                    ATGGTCGGCTTTACCCCCCGTTGCCCCTTGCCGCCTTAGCCGCCACTGGGCCCTTC
                                                  CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAAC
                                                                                                                                                   ATGGTCGGCTTTACCCCCGGTTGCCCTTGCCGGCCTTAGCCGCGACTGGGGCCCTGGCCTTC
                                                                                                                                                                                                                                              983
 CTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAG
                          CACGATGGTTATTACTATTCCTGGTGGAGTGACCGTGGAGCCCACGTACACCAAC
                                                                                                                                                                                           Conservative
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31. .708
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/product= "Endo-1,4-beta-D-xylanase"
/note= "EC-3.2.1.8"
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                                                                                                                                                                                                                                            225 A; 272 C;
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                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                      Score 675; DB 2;
Pred. No. 2.6e-174;
                                                                                                                                                                                                                                              277 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                           Mismatches
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The invention relates to a variant xylanase polypeptide (I) or its fragment having xylanase activity, comprising one or more amino ac
                                                            Novel variant xylanase polypeptide or its fragment useful for degrading or modifying plant cell wall, comprises amino acid modifications such that the polypeptide has altered sensitivity to xylanase inhibitor.
                                                                                                                                                                                        08-MAR-2000;
27-JUN-2000;
                                                                                                                                                                                                                             08-MAR-2001; 2001WO-IB000426
                                                                                                                                                                                                                                                                                                                            Xylanase A; plant cell wall; baking; cereal; starch production; wood; wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.
                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS13813 standard; DNA; 588
                                    Disclosure, Page 64; 70pp; English
                                                                                                               WPI, 2001-596834/67.
                                                                                                                                                                                                                                                      13-SEP-2001
                                                                                                                                                                                                                                                                             WO200166711-A1
                                                                                                                                                                                                                                                                                                      Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                  DNA encoding
                                                                                                                                                                 (DANI-) DANISCO AS
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                                                                                                                                        Sorensen
                                                                                                                                                                                       2000GB-00005585.
2000GB-00015751.
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RESULT 4
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(first

entry)

AAD17927

standard; DNA; 678

ВP

Thermomyces lanuginosus codon optimised xylanase gene

Xylanase; Pichia cell; heterologous nucleotide; codon optimisation;

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Best Local
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                                TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGC
                                                                                                                        CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTAC
                                                                                                                                                                                   CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTAC 633
                                                                                                                                                                                                                                                                                       CGCCAGGACAAGCGCACCAGCGGTACCGGTCCAGACGGGCTGCCACTTCGACGCCTGGGCT 573
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TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGC
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lanuginosus.

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterologous nucleotide sequence encoding a polypeptide of interest, where the codon usage of the sequence has been adjusted to match the preferred codon usage of P. methanolica. The invention also relates to a method for producing high yields of heterologous codon optimised polypeptide in a Pichia cell. The Pichia cell is useful for producing a polypeptide of interest, where the polypeptide is encoded by a nucleotide sequence heterologous to P. methanolica. The present sequence is Thermomyces lanuginosus codon optimised xylanase gene which is the heterologous DNA used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Pichia cell useful for producing polypeptide of interest, a copy of heterologous nucleotide sequence encoding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-2000; 2000DK-00000392
15-MAR-2000; 2000DK-00000419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page
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Pred. No. 2.2e
0; Mismatches
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25-MAR-2003
14-NOV-1995
                                                                                                   A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was isolated from pYES (DSM 6995) and inserted into pHD414 (contg. the TAK promoter and AMG terminator) to form pAXX40-1-1-1. This plasmid and pJaL77 (imparting hygromycin B resistance) were used to transform protoplasts of A. foetidus N0953. The xylanase yield was 0.12 g/l. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ74098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylanase; vector; pAXX40-1-1; Aspergillus foetidus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humicola
                                                                                                                                                                                                          Disclosure; Page 35-36; 47pp; English
                                                                                                                                                                                                                                       of protease or mycotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1993;
                                                           Sequence 1123 BP; 249
                                                                                         correct OS field.)
                                                                                                                                                                                                                                                     Aspergillus foetidus cells expressing heterologous enzyme - partic.
fungal lipase or xylanase, provide high yields without significant
                                                                                                                                                                                                                                                                                                   P-PSDB; AAR75421
                                                                                                                                                                                                                                                                                                                                             Berka RM, Yoder W,
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                35.4%;
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                                                           A; 342 C;
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 Score 239; DB 2;
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                                                           293 G;
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    Indels
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                                                                                                                                                                                                                                                                                                 25-MAR-2003
02-DEC-1995
                                                                                                                                                                                                             Humicola insolens.
                                                                                                                                                                                                                                                                                                                                                                     AAQ94952 standard; DNA; 1123
                 (NOVO ) NOVO
                                           01-DEC-1993;
                                                                       29-NOV-1994;
                                                                                                   08-JUN-1995.
                                                                                                                            W09515391-A2
                                                                                                                                                                                                                                        Xylanase;
                                                                                                                                                                                                                                                                  Humicola insolens xylanase
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                 NORDISK BIOTECH INC
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  ABQ80362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A strain of E. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA fragment is isolated from one of the clones. The sequence of the xylanase gene and protein are given in AAQ94952 and AAR78231 and the gene is deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)
                           ABQ80362 standard; cDNA; 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or mycotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 39-40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus japonicus-type cells expressing heterologous protein - esp. fungal enzyme, provide high yields without significant prodn. of protease
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                                                                                                CTATGTT
                                                                                                                            CACCGTT 663
                                                                                                                                                      CCAGCACTACTACCAGGTCGTCGCCACCGAGGGCTACCAGAGCAGTGGCGAGTCCGACAT
                                                                                                                                                                       TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT
                                                                                                                                                                                                            CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCACGGAATGCCGCT---CGG
                                                                                                                                                                                                                                      TACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
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Pred. No. 4.7e-55;
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enzyme such as tannase, cellulase, glucose vaccoup, phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comporising the tannase are useful for modulating the amount of compounds that comprise a gallate ester linkage in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition. Compositions comprising the amount of glucose oxidase are useful for modulating the amount of myo-inosicol phosphates in a composition. Compositions comprising phytase are useful for modulating the amount of myo-inosicol phosphates in a composition. Compositions comprising beta-galactosidases are useful for modulating the amount of lactose in a composition. Compositions comprising beta-galactosidases are useful for modulating the amount of compositions comprising beta-galactosidases are useful for modulating the amount of formodulating the amount of compositions comprising beta-galactosidases are useful for modulating the amount of compositions comprising the compositions composi
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                                                   polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. funigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A.fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sucrose in a composition. Compositions comprising lipase are useful for modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in ABQ80319-66 encode enzymatic proteins derived from A. fumigatus. The resulting proteins display the catalytic activity of an enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus
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ABQ80364 standard; cDNA; 705

ВP

11-AUG-2003

(first entry

Gene; enzyme; tannase; cellulase;

glucose

oxidase; glucoamylase; phytase;

fumigatus AfXYL2 cDNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 666 BP; 142
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                                                                                         GACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATC
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Pred. No. 3.5
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polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lacicose; tea leaf; sucrose; glyceride; starch, maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability; ss.
Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                          beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
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CBS Location/Qualifiers /product= "Xylanase 2" ø

WO2003012071-A2

13-FEB-2003

05-AUG-2002; 2002WO-US024842

03-AUG-2001; 2001US-0309870P

(ELIT-) ELITRA PHARM INC

Storms R, Roemer H Bussey H;

Novel isolated Aspergillus fumigatus industries such as those involved in beverages, textiles and detergents. polypeptide, useful in the making of food and feed,

Claim 2; Page 165-66; 169pp; English.

CC ester linkage in a composition. Compositions engrising cellulase are compositions comprising glucose oxidase are useful for modulating the amount of cellulose in a composition. Composition. Composition. Composition comprising cellulase are camount of glucose ox oxygen in a composition. Compositions comprising the amount of glucose oxidase are useful for modulating the amount of myo-inositol phosphates cellulase are useful for modulating the amount of myo-inositol phosphates of in a composition. Composition. Compositions comprising beta-galactosidases are useful for modulating the amount of glyceride in a composition. Compositions comprising lipase are useful for modulating the amount of glyceride in a composition. Compositions comprising lipase are useful for modulating the amount of starches or maltodextrins in a composition compositions comprising comprising comprising glaba-samylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising composition composition compositions comprising composition composition composition compositions comprising composition. The amount of night or low molecular weight composition acid chains in a composition. Compositions comprising composition acid chains in a composition. Compositions comprising composition acid chains in a composition. Compositions comprising composition compositions compositio phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccas polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compounds that comprise a gallate The sequences given in ABQ80319-66 encode enzymatic proteins derived from A. fumigatus. The resulting proteins display the catalytic activity of an enzyme such as tannase, cellulase, glucose oxidase, glucosmylase, se oxidase, glucoamylase, lipase, alpha-amylase, laccase,

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Best Local :
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                                                                                                                                GCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGA
                                                                                                                                                                                        GGGGCACTGTCAACACCGACGGTGGCACTTACAACATCTACACGGCCGTTCGCTACAATG
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CTGCTTCCATCACTGT
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                                                      A---CCTGGGAACTCACAACTACCAGATTGTCGCCACTGAGGGTTACCAGAGCAGCGGAT 682
                                                                                ATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCT
                                                                                                             GTACCGGCGCACTGTCACCATGGCCAACCACTTCAACGCCTGGAGCAGACTGGGCATGA
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Pred. No. 2.
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Xylanase; plasmid;
pulp-bleaching; ds.
                                                          Streptomyces
                                                                          27-AUG-2003
01-FEB-2000
                Streptomyces olivaceoviridis
                                                                                                                   AAZ28864
                                                                                                                    standard; DNA; 1195 BP
                                                          olivaceoviridis xylanase (XynG)
                                                                         (revised)
(first entry)
Location/Qualifiers
                                         expression;
                                         E.coli; xylo-oligosaccharide; xylan;
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gene

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pulp-bleaching.
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SEIBUTSUKEI TOKUTEI SANG
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             GACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGGCTCGCGCT
                                                                                                                                                     TCGGGCAGCTTCTACCCGTCCGGCAACGGCTACCTGGCGCTGTACGGGTGGACCTCGAAC
                                                                                                                                                                                                                                                                                                   GCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGC
                                             TACAACGCCCCCTCCGTGGAAGGCACCAAGACCTTCAACCAGTACTGGAGCGTCCGGCAG
                                                                  ACGTACAAGGGCACGGTCACCAGCGACGGCGCGCACGTACGACGTCTACCAGACGACGCGG
                                                                                                           ACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGC
                                                                                                                                        CCGCTCGTCGAGTACTACATCGTCGACAACTGGGGCCAACTACCGGCCCACC-----GGA
                                                                                                                                                                                                                                 GGGAACTTCGTCGCCGGCAAGGGCTGGAGCAACGGCGGACGC--
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/gene= "XynG"
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                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                       Score 205; DB 2; L
Pred. No. 9.5e-46;
0; Mismatches 200;
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ID ANZ2865
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Matches 354
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pulp-bleaching; ds.
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01-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 6-7;
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SEIBUTSUKEI TOKUTEI SANG
                                                                                                            Similarity
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ACCACCAACCAGACCGGCACCAACAACGGGTTCTACTACTCCTTCTGGACCGACGGCGGC
                                       ACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 159
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(first entry)
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418. .990
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/gene= "XynG"
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                                                                                  Score 205; DB 2;
Pred. No. 9.5e-46;
0; Mismatches 200
                                                                                                                                                                          C; 333
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RESULT 11

ADK70798

ID ADK70

XX ADK70

XX ADK70

XX Strep

XX Strep

XX Strep

XX ADK10

PT CDS

PT CDS

PT CDS

PT CDS

PT 14-SE

XX 14-SE

XX 14-SE

XX WPI;

DR WPI;

DR WPI;

DR WPI;

DR WPI;

DR Heat-
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                        WPI; 2003-514374/49.
P-PSDB; ADK70799.
                                                                                                                                                                                                                                                                                                                   Streptomyces olivaceoviridis; xylan enzyme; enzyme; feed additive; animal feed; gene; ds.
Heat-resisting, antiproteinase acidic-neutral xylanase and its gene.
                                                                                                                                                                                                                                                                                          Streptomyces olivaceoviridis
                                                                                                                                                                                                                                                                                                                                                        Streptomyces olivaceoviridis xylan enzyme encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                               ADK70798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCGGCTCCTCCAACCTCACGGT 983
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/product= "xylan enzyme"
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AC ADL23
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes the Streptomyces olivaceoviridis xylan enzyme. The xylan enzyme has good heat stability, high activity under acidic and neutral pH. The xylan enzyme can be used as a feed additive and can be widely used in animal feed.
                                       Aspergillus
                                                                     ss; gene; A. niger; (hemi)cellulase; filamentous fungus; dough; bread; biscuit; elasticity; stability; stickiness; extensibility; machinability; crumb structure; softness; flavour.
                                                                                                                            A. niger (hemi)cellulase NBE021 coding sequence
                                                                                                                                                        20-MAY-2004
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                                                                                                                                                                                                                                                                                     AGCGGCTCCTCCAACATCACGGT
                                                                                                                                                                                                                                                                                                                                            GGCATGCAACTGGGCAGCTTCAGCTACTACATGATCCTCGCCACCGAGGGCTACCAGAGC
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                                         niger.
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Pred. No. 2.1e-45;
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Best Local S
Matches 398
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19-AUG-2002;
19-AUG-2002;
30-AUG-2002;
03-SEP-2002;
03-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                    also useful as query sequences to identified other family members or related sequences. Anti-(hemi)cellulase antibodies are useful for qualitative or quantitative determination of a polypeptide in a biological sample. These antibodies are also useful in diagnosing organism is infected with Aspergillus. The dough prepared by using the inventive (hemi)cellulase has increased strength, elasticity, stability, reduced stickiness, improved extensibility and machinability. The prepared baked product has improved crumb structure, softness and flavour. The (hemi)cellulase has higher specificity towards the substrate, is less antigenic and produces less undesirable side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes an A. niger (hemi)cellulase NBE021. The (hemi)cellulase coding sequences of the invention are derived from a filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase is useful in producing dough, which is useful for preparing a baked product such as bread, biscuits from the dough. Fragments of the (hemi)cellulase DNA are useful as probes and primers for detecting the expression of (hemi)cellulose mRNA in a biological sample such as a tissue. They are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel hemicellulase NBE012, NBE021, NBE022, NBE064, NBE075 or NBE092 derived from Aspergillus niger, useful for preparing dough and/or bal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2003;
                                                                                                                                                                                                                                                                                                                             Sequence
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The invention describes an isolated or recombinant polypeptide having 50% or more identity to 190 300-1200 residue amino acid (S1), given in the specification, over a region of 100 or more and the polypeptide as thermostable xylanase activity. (I) is under the polypeptide of the constable of the constable of the constable to the constable of th

residues useful for: sequences

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Best Local Similarity
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            Aspergillus
                                             17-OCT-2003
22-JUL-1997
                                                                                           AAT63044;
                                                                                                                        AAT63044 standard;
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                                                                                                                                                                                                                       AGCAGCGGCTATGCTCGCATCACCGTTG
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              niger xylanase
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(first en
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59.9%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cDNA clone (AAT63044), deposited as CBS 590.95, codes for a xylanase (AAW14597) of Aspergillus niger N400 (CBS120.49). It was isolated using a method for identifying a DNA fragment encoding a protein of interest. The method involves the direct screening of a cDNA library prepd. in bacterial (e.g. E. coli) transformed with DNA from a eukaryotic organism (e.g. A. niger) that produces the protein. Screening for xylanase-producing clones can be performed on agar plates containing oat spelt xylan and RBB-xylan. The method was utilised in the identification of CDNA clones (AAT63042-46) coding for A. niger cellulase, xylanase and arabinoxylan degrading enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying DNA fragments encoding proteins, e.g. for new enzyme discovery - by direct screening of a cDNA library in bacteria trawith DNA from eukaryotic organism producing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 19-20; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-235889/21.
P-PSDB; AAW14597.
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GCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATCCACT
                                                                                                                                                                                                                                                                                                                                      GAGCGCAGGCCACGTACACCCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATG
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                                                   GCACGTACAAGGGCACCGTCACCTCGGACGGATCCGTTTACGATATCTACACGGCTACCC
                                                                                                                                                                                                       TTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCA
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                                                                                 CTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTC
                                                                                                                  ACCCTCTGATCGAGTACTACATCGTCGAGTCCTACGGCGACTACAACCCCGGCAGTGGAG
                                                                                                                                                  ACAGCGGCACCTTCACCCCTAGCGGCAACGGCTACCTCTCCGTCTATGGCTGGACCACTG
                                                                                                                                                                                                                                                TGGGCAACTTTGTCGGTGGAAAGGGCTGGAACCCCCGG---AAGTGCGCAGGACATCACCT
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Pred. No. 5.5e-44;
0; Mismatches 216;
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16-OCT-2003
25-MAR-2003
28-SEP-1999
has been transformed with a vector encoding a protein having xylanase activity, where the protein comprises an amino acid sequence from a xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481. Also described is an enzyme preparation derived from the culture medium. The enzyme composition can be used in a method for biobleaching, modifying plant biomass properties, especially the reduction of lignin content in pulp and paper processing. The xylanases are hemicellulases which partially degrade the hemicellulose and enhance the extractability of lignins by conventional chemical bleaching of wood pulp. It can be used alone or as a supplement to other treatments that reduce lignin content of wood pulp, increase its drainability or decrease its water retention. The culture medium can be used directly without the need to
                                                                                                                                                                                                                                                                                                                            Fagerstrom R,
Maentylae A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomadura |
thermostable;
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                                                                                                                                                                                 culture of a recombinant
                                                                                                                                                                                                                           Disclosure; Fig 13; 54pp; English.
                                                                                                                                                                                                                                                       Actinomadura xylan sequences and method
                                                                                                                                                                                                                                                                                                                                                                          (ROHG ) ROEHM
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31-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5935836-A.
                                                                                                                                                                              present invention describes a culture medium obtained from the ture of a recombinant host cell that is not Actinomadura flexuosa
                                                                                                                                                                                                                                                                                    1996-141347/38.
DB; AAY24480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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94US-00332412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum and thermostability desirable for the biobleaching of wood pulp reducing the need to acidify the pulp prior to xylanase treatment. The xylanases partially degrade the hemicellulose in wood pulp which enhances the extractability of lignins by conventional bleaching chemicals and results in a lower consumption of bleaching chemicals reducing the formation of environmentally undesired organic compounds. The present sequence encodes actinomadura sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed from US5935836 which is a treat as basic specification for FI9503639. (Updated on 25-MaR-2003 to correct DR field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1375 BP; 265 A;
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997
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Search completed: February 11, Job time : 423.587 secs 2006, 18:30:53

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Result
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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ALIGNMENTS

	Bource	FEATURES		COMMENT	JOURNAL	TITLE	AUTHORS	A DATE OF THE PARTY OF THE PART	aowagaga	ORGANISM	SOURCE	SUBORARA	ACCESSION	DEFINITION	Locus	RESULT 1 DR637934
/organism="Gibberella moniliformis" /mol type="mgNA" /strain="m3125" /db xref="taxon:117187" /clone="FVMB275" /tissue type="mycelia" /clone lib="FvM" /clone lib="FvM" /site 2: XhoI; anamorph: Fusarium verticillioIdes. Library site 2: XhoI; anamorph: Fusarium verticillioIdes. Library rom was prepared from pooled RNA obtained from a 48-hour and a 72 hour, liquid GYAM culture from strain M-3125. Cultures were vacuum filtered and the mycelial mats were frozen in liquid nitrogen, ground to a powder, and then added to TRIIOl Reagent (Invitrogen, Carlabad CA) at approximately 1 g mycelia per 10 ml TRIZol. The cDNA was	1860	USDA 1815 N. University St, Peoria, IL 61604, USA Tel: 309 681 6230 Fax: 309 681 6689 Email: browndw@ncaur.usda.gov TIGR sequence name: FVMB275TH Seq primer: AAT TAA CCC TCA CTA AAG GG. Location/Qualifiers	USDA/ARS/NCAUR	Contact: Brown, D.W.	<pre>spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)</pre>	Analysis of 87,000 expressed sequence tags reveals alternatively	Utterback, T., Smith, S., Feldblyum, T., Glenn, A.B., Plattner, R.D.,	Denotor B II Butoble & E Those I		Gibberella moniliformis	Gibberella moniliformis		DR637934 1 GI-70712768	EST1028559 FvM Gibberella moniliformis cDNA clone FVMB275, mRNA		

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Gibberella moniliformis

Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 883)

1 (bases 1 to 883)

Brown, D.W., Cheung, F., Procttor, R.H., Butchko, A.E., Zheng, L. Lee, Y. Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Kandra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D.W.
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EST1033915
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                                   CTTCGACGCCTGGGAGAAGGCTGGTATGAAGCT----CGGTACCCACGACTACCAGATCCT
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Query Match
Best Local Similarity
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USDA
1815 N. Univers
Tel: 309 681 62
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TIGR sequence name: FVMCX47TH
Seq primer: AAT TAA CCC TCA C'
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Fax: 309 681 6689
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CTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGT
                                                          GCAGTACTGGTCTGTTCGCCAGCAGCATCGCTCTACTGGTAGCGTTGACACTGGTCTTCA
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/notes TypelueScript II SK(+) XR; Site 1: EcoRI;
/notes TypelueScript Fusarium verticillioides. Library
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FyM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIZOl. The CDNA was
directionally ligated into the plane Tript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
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/clone_lib="FvM"
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/clone="FVMCX47"
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/strain="m3125"
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DR037502
DR037502.1 GI:66839397
EST.
Solanum tuberosum (potato)
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1 (bases 1 to 882)

Flint, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S Generation of ESTs from late blight-challenged potato tubers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Canadian Potato Genome Project 921 College Hill Rd, Fredericton, (Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Barry Flinn
                                                                                                                                                                                                                                                                                     Similarity
                                                                                    CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAAC
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illarity 60.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                 /clone lib="Late Blight-Challenged Tubers"
//notes "Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
/notes "Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Tubers"
/lab_host="XL10-Gold"
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Contact: Barry Flinn
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The Canadian Potato Genome Project 921 College Hill Rd, Fredericton, C Email: bflinn@bioatlantech.nb.ca
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Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., Flinn, B., Lague, M., L
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EST.
Solanum tuberosum (potato)
Solanum tuberosum
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/tissue_type="Tubers"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
/clone_tib="Late Blight-Challenged Tubers"
/clone_tib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
/note="Vector: pBluescript II SK(+) XR; Site_1: Tubers
/note="Vector: pBluescript II SK(+) XR; Site_1: Tubers
/row pathogen-free Solanum tuberosum var. Shepody, clone
/row pathogen-free Solanum var. Shepody, clone
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RESULT 5
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             1 (bases 1 to 744)
Diener, S.B., Dunn-Coleman, N.,
Teunissen, P.J.M., van Solinge
                                                                Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pe
Hypocreomycetidae; Hypocreales;
                                                                                                                                                                                        CF867983 744 bp mRNA linear EST 31-OCT-2003 tric013xe09.bl T.reesei mycellal culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric013xe09, mRNA sequence.
                                                                                                                                                                                 Hypocrea jecorina
CF867983
Ward, M. and Dean, R.A.
                                                                                                                        Hypocrea jecorina
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ilarity 60.9%;
Conservative
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                                                                                                                                                              GI:38122635
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Pred. No. 1.2e-53;
0; Mismatches 251;
                Solingen, P.,
                                                                                                                        Trichoderma
                                 Foreman, P.,
                                                                                    Pezizomycotina;
                                                                   Hypocreaceae;
               Dankmeyer, L.,
                                 Houfek, T
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                  Mitchell, T.K.,
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Seq primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27
Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ralph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett.
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ACTACCAGATCGTTG-CAACGGAGGGCTACTTCAGCAGCGGCTATGCTC
                                                                                                                                    CCGCCACCTTTTACCAGTACTGGTCCGTCCGCCGCAACCACCGCTCGAGCGGCTCCGTCA
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                                                                                     <u>AGACGGGCTGCCACTTCGACGCCTGGGCTCGCCGCTGGTTTGAATGTCAACGGTGACCACT</u>
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture,
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/mol_type="mRNA"
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Pred. No. 2.1e-52;
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12788920
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925 Page Mill Road, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      799 ktric013xe09 T.reesei mycelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        filamentous fungus
J. Biol. Chem. 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypocrea jecorina (anamorph: Trichoderma
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                                                                                                                                          CCGGCGGGCAGTTCTCCGTCAACTGGGTCCAACTCGGGCAACTTTGTCGGCGGCAAGGGAT
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ACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCCTGATCGAGTACTACATCGTCG
                    ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCG
                                                                                                     GGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCA
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(650) 621-7817
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/note="Vector: pREP3Y; Site_1: Not ISA1 I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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/mol_type="mRNA"
/strain="QM6a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 229; DB 6;
Pred. No. 2.1e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science, plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
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Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
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Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 706 542 1860
Fax: 706 583 0210
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Contact: Cordonnier-Pratt MM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                      primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
/clome="OXI 9 D10 A002"
/clome="DXI 9 D10 A002"
/clome lib="OXidatively-stressed leaves and roots"
/clome lib="Oxidatively-stressed leaves and roots"
/note="Oxgan: Leaf and Root; Vector: PME18S-FL3; Site_1:
XhoI; Site_2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                              organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                 lon/Qualifiers
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, I Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; G 1 (bases 1 to 639)
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EST1015056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTACTCTTGGTGGTCTGATGGCGGTGGCTATGCCAACTATCAGATGGGTGAGGGAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the MME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the insert."
                                                                                                                                                                                     moniliformis
                                                                                                                                                                                                                                                                                       FvI Gibberella
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Pred. No. 1.2e-50;
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FVIBB05, mRNA
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1815 N. University
Tel: 309 681 6230
Fax: 309 681 6230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIBB05TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                       ACTATTCCTGGTGGAGTGACGGTGGAGCCCACGCTACACCCAACCTGGAAGGCGGCA 193
                                                                                                                                                                                                                                                                                                                                                          CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                                                                                                                                        GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA
                                                                                                                                                                                                                                                                                                    GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACC
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                   GCCACTTCGACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
                                                                                                             CCTATGATCTGTACCAGACCACCCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                  TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT
                                                                                                                                                                 GCACTTACAATCCCGGCTCTGCTGGCCAGCACAAGGGCACCGTCTACAACGACGGCGACA
                                                                                                                                                                                                                                                                            G---TACTGGCCGAACTATCAACTATGGCGGTTCTTTCAGCCCTCAGGGTAACGGCTATC
    CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA
                                                       TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGGCGCTGTCAACATGCAGA
                                                                              TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
                                                                                                                                                                                                                       TCTGCGTCTACGGCTGGACCCGCAGCCCTCTCGTCGAGTACTACGTCATCGAGAACTACG
                                                                                                                                                                                                                                                  TTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTG
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/clone_lib="FvI"
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/clone="FVIBB05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 220.4; DB 8; Pred. No. 4.9e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Vutterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A., Analysis of 87,000 expressed sequence tags reveals alternatively
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1 (bases 1 to 749)
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EST1013225
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TIGR sequence name: FVIAM2ZTH
Seq primer: AAT TAA CCC TCA CTA AAG
Location/Qualifiers
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes **Westor: pBlueScript II SK(+) XR; Site 1: EcoRI; /notes **Vestor: pBlueScript II SK(+) XR; Site 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioIdes. Library FvI was prepared from growth on excised maize seedling roots and shoots. The roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 10e6 conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman
                                                                                                                                                                                                                                                                                                                                                  #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIZOl Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOl. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="mycelia"
clone_lib="FvI"
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|strain="m3125"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB801TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 309 681 6230
Fax: 309 681 6689
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Contact: Brown, D.W.
USDA/ARS/NCAUR
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Brown, D. W., Cheung, F., Proctor, R. H., Butchko, A. E., Zheng, L., Lee, Utterback, T., Smith, S., Feldblyum, T., Glenn, A. E., Plattner, R. D., Kendra, D., Town, C. D. and Whitelaw, C. A.

Kendra, D. F., Town, C. D. and Whitelaw, C. A.

Analysis of 87,000 expressed sequence tags reveals alternatively
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/tissue_type="mycelia"
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/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
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Brown, D. W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Ytterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; (1 (bases 1 to 719)
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Email: browndw@ncaur.usda.
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USDA/ARS/NCAUR
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        CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA
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                                                                                                                                                                       TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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R sequence name: FVIEA21TH
primer: AAT TAA CCC TCA CTA
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/EISBUE TYPE="Mycelia"
/Lione Tib="FVI"
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/Clo
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/strain="m3125"
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/clone="FVIEA21"
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Pred. No. 9.5e-50;
0; Mismatches 211;
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1 (bases 1 to 733)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIDX40TH
Seq primer: AAT TAA CCC TCA CTA AAG
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                                                                                                                                                                                                                                                       CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 133
                                                                                      TCTACTCTTGGTGGTCTGATGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="mycelia"
/clone Tib="PVI"
/clone Tib="Color: pBlueScript II SK(+) XR; Site 1: EcoRI;
/clone Tib="Color: pBlueScript II SK(+) XR; Site 1: EcoRI;
/clone Tib="Color: pBlueScript II SK(+) XR
/clone Tib="Col
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/strain="m3125"
/db_xref="taxon:117187"
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Pred. No. 9.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                        Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB280TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 739)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 N. University
: 309 681 6230
: 309 681 6689
/tissue type="mycelia"
/tissue type="mycelia"
/clone_Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Librar
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Librar
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly i
                                                                                                                                                                                            /db_xref="taxon:117187"
/clone="FVIB280"
                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="m3125"
                                                                                                                                                                                                                                                                                              organism="Gibberella
                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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DR625790
                                                                                    REFERENCE
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                                                                 AUTHORS
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Utterback, T., Smith, S., Feldblynm, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals alternatively
                                                                                                                              Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                           DR625790
EST1015918
                                                                              Hypocreomycetidae, Hypocreales, 1 (bases 1 to 741)
                                                                                                                                                                       Gibberella moniliformis
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                                                                                                                                                                                                                                                                             741 bp mRNA linear FvI Gibberella moniliformis cDNA clone
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63.2%;
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Pred. No. 9.5e-50;
                                                                                                          Nectriaceae;
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                                                                                                          Gibberella.
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Unpublished (2005)
Contact: Brown, D.
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Fax: 309 681 6689
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GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
                                                                                                                                                                                                               CCTATGATCTGTACCAGACCACCCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                                                                                                                                                                 TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G---TACTGGCCGAACTATCAACTATGGCGGTTCTTTCAGCCCTCAGGGTAACGGCTATC
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                                                                                                                TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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R sequence name: FVIBR33TH
primer: AAT TAA CCC TCA C
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/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
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/strain="m3125"
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Pred. No. 9.5e-50;
0; Mismatches 211;
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Query Matcl Best Local Matches 3 Qy 7 Db 15 Qy 13 Db 21	ORIGIN	FEATURES Bource	TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	SULT 15 624330 CUS FINITION	9D 4G
tch 32.5%; Score 219.4; DB 8; Length 763; al Similarity 63.2%; Pred. No. 9.6e-50; 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2; 74 CCACGGAGCTCGAAAAGCGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 133	/organism="clubergila monilirormis" /mol type="mRNA" /strain="m3125" /db_xref="taxon:117187" /clone="FVLB212" /clone="FVLB212" /tissue_type="mycelia" /clone="FVCtor: pBlueScript II SK(+) XR; Site_1: EcoRI; Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library FvI was prepared from growth on excised maize seedling roots and shoots for roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 10e6 conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (CDNA Synthesis Kit; Stratagene)."	USDA 1815 N. University St, Peoria, 1815 N. University St, Peoria, Tel: 309 681 6230 Fax: 309 681 6689 Email: browndw@ncaur.usda.gov TIGR sequence name: FVIB212TH TIGR sequence TCA CTCA CTCA CTCA CTCA CTCA CTCA CTCA	.um,T., Glenn,A.E., Plattner,Relaw,C.A. guence tags reveals alternati ses of the fumonisin gene clus	tina; Sord eae; Gibbe chko,A.E.,	TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662	602 CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACTTGGAAACCACTACTATCAGA 658

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                                                           631 CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA 687
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                                                                                    GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 613
                                                                                                                                       TCGACCAATACTGGTCCGGTCCGGCAGGACAAGCGCACCCAGCGGGTACCGTCCAGACGGGCT 553
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                                                                                                                     TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCGGCGCGCTGTCAACATGCAGA 630
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Search completed: February 11, 2006, 20:39:41 Job time : 3419.97 secs

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Result
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-09-735-832-1
US-09-254-733-1
US-09-121-436A-1
US-09-121-436A-1
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RESULT 1

ALIGNMENTS

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US-08-104-445-1	US-08-104-445-2	US-09-603-311-23	US-09-390-234-23	US-08-121-436A-3	US-07-842-349-1	US-09-595-344-1	US-08-315-695-15	US-09-260-283-1	US-09-189-060B-46	US-08-244-686-1	US-07-955-726A-7	US-09-367-891A-4	US-09-613-811-5	US-08-981-729-5	US-08-963-500-2	US-08-575-964-2	US-09-189-060B-11	US-09-970-616-1	US-09-230-590-1	US-09-462-246-1
Sequence 1, Appli	Sequence 2, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 46, Appl	Sequence 1, Appli	Sequence 7, Appli	Sequence 4, Appli	Sequence 5, Appli	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

US-08-886-765-1 ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 4324 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 TELEPAX: 212-879-9655 INFORMATION FOR SEQ ID NO: 1: GENERAL INFORMATION: APPLICANT: Hansen, APPLICANT: Wagner, APPLICANT: Mullertz Sequence 1, Application US/08886765 Patent No. 5817500 SEQUENCE CHARACTERISTICS: LENGTH: 983 base pairs TYPE: nucleic acid STRANDEDNESS: single ZIP: 10174 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette APPLICANT: Knap, Inge Helmer TITLE OF INVENTION: Animal Feed Additives NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: No. 58175000 No. 5817500disk of No. 5817500th America, Inc. MOLECULE TYPE: ORIGINAL SOURCE: COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: FEATURE: NAME/KEY: LOCATION: ORGANISM: STRAIN: D APPLICATION NUMBER: US/08/886,765 FILING DATE: 1-JUL-1997 STREET: 405 Lexington Avenue CITY: New York STATE: NY TOPOLOGY: COUNTRY: CLASSIFICATION: DSM 4109 USA Wagner, Peter Mullertz, Anette Hansen, Peter Kamp linear Thermomyces lanuginosus 33,728 ER: 4324.204-US

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Best Local Similarity
                                                                                                                                                                                                                       GENERAL INFORMATION:
STREET: 40
STREET: NEW YORK
STATE: NY
COUNTRY: USA
COUNTRY: 10174
                                                                                     APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Wallertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6245546disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                               601
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                                                                           405 Lexington Avenue
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: cl
ORIGINAL SOURCE:
ORGANISM: Ther
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NAME/KEY:
LOCATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESE FOR Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: DSM 4109
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                                  GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACC
                                                                                                  TGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGAC
                                                                                                                                             GTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAG
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                  GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCA
                                                                              TGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGAC
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US-08-458-023B-3
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                                                                                           Best Loc
Matches
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                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 212-8/0-701
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31.274
REFERENCE/DOCKET NUMBER: 4086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                              MOLECULE NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
TYPE: internal
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APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan C.
APPLICANT: Takagi, Shinobu
APPLIC
                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
ORGANISM: Humicola
INDIVIDUAL ISOLATE:
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STATE: New York
                                                                                                                                                                                                                   LOCATION:
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CGTTCCTCGGGACAACTCGACGGCCCTTCAGGCTCGACAGGTGACCCCCAACGGCGAGGG
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llarity 64.4%;
Conservative
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ISOLATE: DSM 6995
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                                                                                         Score 239; DB 2; Length 1123; Pred. No. 3.2e-57; Indels 0; Mismatches 210; Indels
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                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/468,812
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Actinomadura Xylanase Sequences TITLE OF INVENTION: of Use NUMBER OF SEQUENCES: 25
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  FILING DATE:
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Suominen, Pirkko
Lahtinen, Tarja
Kristo, Paula
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994

08/332,412

CLASSIFICATION:

FILING DATE: 3: CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
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LOCATION:
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STRANDEDNESS: not relevant
TOPOLOGY: linear
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Pred. No. 3.5e-45;
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Query Match
Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNBY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
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APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion
                                                                                                                  FEATURE:
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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                                                                                 NAME/KEY:
LOCATION:
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                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: not relevant
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1100 New York Ave., N.W. Suite 600
                                                                                                                                                                                                  1375 base pairs
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Score 196.2; DB 3;
Pred. No. 3.5e-45;
0; Mismatches 263;
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APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OP INVENTION: Production ar
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: M ntyl
STREET: 1100 New York Ave., N
CITY: Washington
STATE D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                   ADDRESSEE:
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                                                                                                   E: STERNE, KESSLER,
1100 New York Ave.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
FEATURE:
NAME/KEY: CDS
LOCATION: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                            ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCA 484
                    ACGGGGGAACGTACGACATCTACGAGACCTGGCGGTACAACGCGCCGTCCATCGAGGGCCA
                                                                         AGAGCTGGGGCACCTACCGGCCCACCGGC
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
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CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0160
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 31-OCT-
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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SOGTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
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APPLICATION NUMBER: US
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                                                                                                       ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGGTGGTCGAGTATTACATCGTCG
                                                                                                                                                     GGTCCACCGG----GGGACGGGGACCGTGACCTACAACGCCTCCTTCAACCCCGTCGGGTA
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                                                            ACGGCTACCTCACGCTCTACGGCTGGACCAGGAACCCCGCTCGTCGAGTACTACATCGTCG
                                                                                                                                                                                                                                                                                                                                          ACGGCTACTTCTACTCGTTCTGGACCGACGCCCCGGGACCGTCTCCATGACCCCTCCACT
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Pred. No. 3.5e-45;
0; Mismatches 263
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US-09-235-832-1
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
TOPOLOGY: 1
MOLECULE TYPE:
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                           REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Wa
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
           TYPE: nucleic acid
STRANDEDNESS: No. 6667170 Relevant
TOPOLOGY: linear
                                                                                                                                                  NAME: Bugaisky, Lawrence B. REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    LENGTH:
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                                                    1375 base pairs
                                                                                                202-371-2540
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Fagerstr m, Richard
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(genomic)
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US-09-235-832-1
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US-09-254-733-8
GENERAL INFORMATION:
APPLICANT: WATANABU
APPLICANT: WATANABI, MANABU
APPLICANT: MOTANA, TATSUKI
APPLICANT: MOTANA, TAKUKI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*LC(MMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09254733 Patent No. 6277596
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGAGGGTGGC 1007
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RESULT 9
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Patent No. 563/312)

GENERAL INFORMATION:

APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena

APPLICANT: Nevalainen, Ritva

APPLICANT: Saarelainen, Ritva

APPLICANT: Paloheimo, Marja

APPLICANT: Lahtinen, Tarja

APPLICANT: Fageretr m, Richard

ITITLE OF INVENTION: No. 58375151 Enzyme Preparations and Methods

ITITLE OF INVENTION: for Their Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                        Sequence 1, Application US/08121436A Patent No. 5837515
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Best Local
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SOPTWARE: PatentIn Ver. :
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NAME/KEY:
LOCATION:
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LOCATION:
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NAME/KEY: Big_peptide
LOCATION: (14)..(112)
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TYPE: DNA
ORGANISM: TRICHODERMA VIRIDE MC300-1
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Pred. No. 1.1e-44;
0; Mismatches 123;
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Best Local Similarity
Matches 278; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/F193/
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889
FILING DATE: 29-MAY-1992
PRIOR APPLICATION NUMBER: US 07/524
APPLICATION NUMBER: US 07/524
FILING DATE: 16-MAY-1990
APPORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEBONE: (202) 371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
NAME/KEY:
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LENGTH: 1015 base pairs
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PRIOR APPLICATION DATA:
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TELEPHONE: (202)
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nilarity 68.5%;
Conservative (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/078,478 FILING DATE: 18-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      546 TAAAAAAAAAGGGTCATCAACTTCTCGGGAAGCTACAACCCCAACGGCAACAGCTACCTCT 605
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                              ACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCC
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                                                                                                     ACGACATTTACCGCACGCAGCGCGTCAACCAGCCGTCCATCATCGGCACCGCCACCTTTT 785
                                                                                                                                                      ATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCG
ACCAGTACTGGTCCGTCCGCCGCAACCACCGCTCGAGCGGCTCCGTCAACACGGCGAACC
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1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(176..448, 557..952)
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RESULT 10
US-08-768-373-1
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                                                                     NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION:
US-08-768-373-1
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 Best Loc
Matches
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GENERAL INFORMATION:
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (202) 371 2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
                                                                                                                                                                                                                                               TOPOLOGY: line:
MOLECULE TYPE: DI
ORIGINAL SOURCE:
ORGANISM: Chae:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LAHTINEN, TARJA
APPLICANT: PAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                          FEATURE:
 Local Sinth
                                                                                                                                                                        NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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FILING DATE: 17-DEC-1996
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                                                                                                                                                            OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                  Similarity
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VEHMAANPER , JARI
LANTTO, RAIJA
     Conservative
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195..423
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                  26.9%;
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Score 181.8; DB 3
Pred. No. 3.8e-41;
0; Mismatches 147
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                                DB 3;
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US-09-849-242A-1
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GENERAL INFORMATION:
                                                                                                                                                                            ZIP: 20005-3934
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                         APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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STREET: 1100 NEW YORK AVENUE, SUITE
CITY: WASHINGTON
STATE: DC
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 FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
                                                  APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
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INVENTION: NOVEL XI
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VEHMAANDERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTRIM, RICHARD
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IOCATION: 483..1039

LOCATION: 483..1039

OTHER INFORMATION: /product=
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-849-242A-1
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US-07-744-570B-1
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                                             Sequence 1, Application US/07744570B Patent No. 5202249
GENERAL INFORMATION:
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                 APPLICANT:
    APPLICANT:
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ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 195..423
OTHER INFORMATION:
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Morosoli,
Shareck, F
ם א
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202) 371-2540
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Pred. No. 3.8e-41;
0; Mismatches 147;
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FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Xylanase for Biobleaching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 24.9%;
Local Similarity 60.0%;
nes 343; Conservative
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STREET: 1200 South 47th Stree
STREET: Box Number 4023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
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                            TACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                           GCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGC
                                                                                                                             CAGTCGAAGGTGACCAGTGGCTCCGGCACCATCACCACCGGCAACCACTTCGACGCCTGG
                                                                                                                                                          CAGGACAAGCGCACCAG-----CGGTACCGTCCAGACGGCTGCCACTTCGACGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAACCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGT 156
TATCAGAGCAGTGGAAGCTCGAACATCACGGT
                                                             ĠĊĠĊĠĊĠĊĠĠĠĊAŤĠĂĂĊĂŤĠĠĠĊĊĀĠŦŢĊĀĠĠŤĂĊŤĂĊĀŢĠĂŤĊĂŤĠĠĊĊĂĊĊĠĂĠĠĠĊ
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Pred. No. 1.7e-37;
0; Mismatches 211;
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LOCATION:
US-08-507-431-5
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56935180 No. 5693518disk of No. STREET: 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
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                                                                                               197
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                                                                                                                                                                        137 ATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCT 196
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                                                                                                                                                                                                                                                                                         346;
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TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC----AAACGGCAACAGCTAC 312
                                                                                                                                    GCTTCTGGACCGATGGCGCAAGCGGCGATGTTGAATACAGCAACGGCGCCGGGGGGTCCT
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                                                                                             ACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCC 256
                                                           ACAGCGTGACCTGGTCATCGGCCTCGAACTTCGTCGGTGGAAAGGGCTGGAACCCTGG-A
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Andersen, Luca
et, Joan Q.
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Dalboge, Henrik
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Christgau, Stephan
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                                                                                                                                                                                                                                                                                       Score 164.6; DB 2;
Pred. No. 2.3e-36;
0; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Munk, Niel APPLICANT: Mullertz, TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: AGY16 Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 30-July-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 58858190 No. 5885819disk of No. STREET: 405 Lexington Avenue, 64th Floor
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 TGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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                                                                                           212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mullertz, Anette
VENTION: ENZYMES WITH XYLANASE ACTIVITY
VENTION: ASPERGILLUS ACULEATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Si, Joan Q.
Jacobson, Tina
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Heldt-Hansen, Hans
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                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Kofod, Lene V.

APPLICANT: Kofod, Lene V.

APPLICANT: Christgau, Stepl

APPLICANT: Heldt Hansen, H

APPLICANT: Dalboge, Henrik
                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09116622 Patent No. 6080567
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                                                                                                                      APPLICANT:
APPLICANT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60805670 No. 6080567disk of STREET: 405 Lexington Avenue, 64th Ploor
                                                            APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Munk, Niels
APPLICANT: Munk, Niels
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                        APPLICANT:
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LOCATION:
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                                                                                                                                    Andersen, Lene N.
Si, Joan Q.
Jacobson, Tina
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Christgau, Stephan
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Pred. No. 2.3e-36;
0; Mismatches 239
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                    6080567th America,
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SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
LENGTH: public acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 39:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New IULA
COUNTRY: United States
ZIP: 10174-6401
ZIP: TOTE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 16-Jul CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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     ATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGC 665
                                    AACCATTTCAATGCCTGGGCGAAGCTGGGAATGAATCT---GGGCACGCACAACTATCAG
                                                                   TGCCACTTCGACGCCTGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAG
                                                                                                                         TTCGACCAATACTGGTCCGCTCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGC
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                                                                                                      TTCACGCAGTACTGGTCCATTCGCCAGACAAAGCGCGTCGGCGGTACCGTGACGACTGCC
                                                                                                                                                                      ATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACC
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Db 670 ATCGTCGCTACTGAAGGCTACTACTCGTCTGGGTCTGCGTCCATTACGGTTGC 722

Search completed: February 11, 2006, 20:45:51

Job time: 149.191 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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US-10-425-13-990-68
US-10-213-990-68
US-09-770-621-1
US-10-213-990-67
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US-10-213-990-71
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US-10-213-990-64

US-10-213-990-70

US-11-018-645-21

US-10-213-990-70

US-10-307-441-39

US-09-790-070A-8

US-10-299-393-1

US-11-154-793-1
                    US-09-970-616-1
US-10-765-716-1
US-09-149-310-31
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Sequence 1, Appli
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Sequence 64, Appl
Sequence 71, Appl
Sequence 70, Appl
Sequence 70, Appli
Sequence 39, Appli
Sequence 1, Appli
Sequence 17, Appli
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Sequence 3, Appli
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Sequence 177283,
Sequence 82922, A
Sequence 37173, A
Sequence 65, Appl
Sequence 61, Appl
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Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette
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10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.7	10.7	10.7	11.6	11.6	12.0	12.2	12.2	12.4	13.2	13.4	14.0	15.1	L5.3
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Sequence 10, Appl	Sequence 12, Appl	Sequence 6, Appli	Sequence 12, Appl	Sequence 6, Appli	Sequence 11, Appl	Sequence 10, Appl	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 3, Appli	Sequence 15625, A	Sequence 4, Appli	Sequence 4, Appli	Sequence 48309, A	Sequence 19, Appl	Sequence 15, Appl	Sequence 13, Appl	Sequence 39, Appl	Sequence 5, Appli

ALIGNMENTS

TITLE OF INVENTION: Animal Feed Additives NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CONDENCE: No. US20020160080A1disk of No. US200201600 STREET: 405 Lexington Avenue CITY: New York STATE: NY COUNTRY: USA COMPUTER: NW COUNTRY: USA COMPUTER: PROM: MEDIUM TYPE: Diskette COMPUTER: END Compatible OPERATING SYSTEM: DOS CURRENT APPLICATION NUMBER: US/09/467,368 FILING DATE: 21-Dec-199 CLASSIFICATION NUMBER: US/09/467,368 FILING DATE: 1-UL-197 ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J REPERANCE/DOCKET NUMBER: 33,728 REPERANCE/DOCKET NUMBER: 33,728 TELECHMUNICATION INFORMATION: TELEPHONE: 12-867-0123 TELECOMMUNICATION: TELEPHONE: 212-867-0123 TELEPHONE: 116-87 TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: CNAA ORGANISM: Thermomyces lanuginosus

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Best Local S
Matches 675
                                                                 Sequence 9, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
 APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OP INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
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SEQUENCE DESCRIPTION:
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Pred. No. 3.3e-203;
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Sequence 3, Application US/09803454

Publication No. US20030022280A1

GENERAL INFORMATION:
APPLICANT: No. US20030022280A10zymes A/S
APPLICANT: Takagi, Shinobu

APPLICANT: Terui, Yuri

TITLE OF INVENTION: High Expression of Industrial Enzymes
FILE REFERENCE: 6125.200-US
CURRENT APPLICATION NUMBER: US/09/803,454
CURRENT FILING DATE: 2001-03-09
NUMBER OF EXG ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOPTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-10-237-386-9
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Best Local :
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                                                                                       CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTAC 633
                                                                                                                      CGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCT
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Pred. No.
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8.5e-174;
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Sequence 177283, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
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TYPE: DNA
ORGANISM: Artificial S
PEATURE:
OTHER INFORMATION: Syr
IS-09-803-454-3
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Pred. No. 4.1e-107;
0; Mismatches 189;
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                                             Other Molecules
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RESULT 5
US-10-425-115-82922
US-10-425-115-82922
Sequence 82922, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 177283
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clo.
US-10-425-115-177283
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Pred. No. 7.6e-71;
0; Mismatches 228;
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and

Other

Molecules

Associated With

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RESULT 6
US-10-425-115-37173
Sequence 37173, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La ROBA, Thomas J.
APPLICANT: Kovalic, David K.
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Best Local Similarity
Matches 423; Conserv
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SEQ ID NO 82922
LENGTH: 749
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(749)
OTHER INFORMATION: un
FEATURE:
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GT 732
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Pred. No. 1.7e-67;
0; Mismatches 230;
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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecul;
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,11:
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEO ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea may8
; FEATURE:
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                                                                                                            | CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC
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                       ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                               AGACGGGCTGCCACTTCGACGCCTGGCTCGCCTGGTTTGAATGTCAACGGTGACCACT
                                                                                              CAAGGACCTTTCAGCAGTACTGGTCTGTTCGCCAGAACAAGCGCTCCAGCGGATCCGTGA
                                                                                                                                             AGAACTTCGGAACCTATGACCCGAGTTCCCCAGGCTAGCAACAAGGGTACCGTGACTGCCG
                                               ACATGAAGACTCACTTCGATGCTTGGGCCAGCAAGGGCATGACTCT
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Pred. No. 1.6e-65;
0; Mismatches 241;
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RESULT 7
US-10-213-990-65
; Sequence 65, Application US/10213
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Jiang, Bo
; APPLICANT: Storms, Reg

US/10213990

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APPLICANT: ROEMER, TERTY
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUM
TITLE OF INVENTION: ENZYMES AND METHODS OF USB
FILE REFERENCE: 10.82-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 65
LENGTH: 666
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
RESULT 8
US-10-213-990-68
; Sequence 68, A

// NAME/KEY: CDS
// LOCATION: (1)...(666)
US-10-213-990-65

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                                                                                                                           GACCACTACCAGATCGTTGCAACGGAGGGGCTACTTCAGCAGCGGCTATGCTCGCATC
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                                                                                                           AACTTTGACTATATGATTGTTGCGACGGAGGGGTACCAGAGCAGCGGCTCTGCTACTATC
                                                                                                                                                          ACTGTGACGACGAAGAACCACTTTGATGCGTGGAGAAATGCGGGTCTGCAATT---GGGG
                                                                                                                                                                          ACCGTCCAGACGGCCTGCCACTTCGACGCCTGGGCTCGCCTTGGTTTGAATGTCAACGGT
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Pred. No. 1.5e-60;
0; Mismatches 249;
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 CTGCTTCCATCACTGT
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; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION UNMERS: US/10/213,990
; CURRENT APPLICATION UNMERS: US/10/213,990
; CURRENT PILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; ELNGTH: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.8%;
Best Local Similarity 60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(705)
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ATGCTCGCATCACCGT
                                                                                             ATGTCAACGGTGACCACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCT
                                                                                                                                                                GTACCGGCGCACTGTCACCATGGCCAACCACTTCAACGCCTGGAGCAGACTGGGCATGA
                                                                                                                                                                                             GCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCCTGGGCTCGCGCTCGGTTTTGA
                                                                                                                                                                                                                                                                            CTCCCTCCATCGAAGGCACCAAGACCTTCACCCAGTACTGGTCTGTGCGCACCTCCAAGC
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Pred. No. 1.4e-59;
0; Mismatches 249;
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US-09-770-621-1
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Patent No. US20010024815A1
GENERAL INFORMATION:
                                                                                          Matches 396;
                                                                                                       Best Local
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIA Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/770,621
FILING DATE:
                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:

NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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APPLICANT:
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APPLICATION NUMBER:
FILING DATE:
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TITLE OF INVENTION: Production and Secretion of Proteins
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 29-JUL-199
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994
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                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                           TELEPHONE: 202-371-2540
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACG
                                        TCGGCCTCCGGCGCATCGTCACCAGTGCCTTCGCCCTGGCACTCGCCATCGCCGGTGCGC
                                                                 TCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGG 64
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1100 New York Ave.,
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Suominen, Pirkko
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Fagerstr m, Richard
                                                                                          Conservative
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                                                                                                                                                                                               DNA (genomic)
                                                                                                       29.1%;
59.0%;
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                                                                                        pred. No. 1.8e.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1
                                                                                                       .2; DB 3;
1.8e-51;
                                                                                          263;
                                                                                                                 Length 1375;
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                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10286993 Publication No. US20030148453A1
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      APPLICANT: Mantyla, Arja
APPLICANT: Paloheimo, Ma
APPLICANT: Lantto, Raij
                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                    APPLICANT:
                             TYPE: DNA
                                     LENGTH: 1375
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Suominen, Pirkko
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                                                                                                                                                                                                                                                                            Richard
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APPLICANT: Vehmanipera, Jari
TITLE OF INVENTION: Production and Secretion of
TITLE OF INVENTION: Fungi
FILE REFERENCE: 1716.0340004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/99/120,804
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US/97/00037
PRIOR APPLICATION NUMBER: PCT/F197/00037
PRIOR APPLICATION NUMBER: PCT/F197/00037
PRIOR APPLICATION NUMBER: US/990,563
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
OURSELOW: 1997-01-26
NUMBER OF SEQ ID NOS: 18
ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
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APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-99
CURRENT APPLICATION NUMBER: 990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                      RESULT 11
US-10-213-990-67
; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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; LOCATION: (303)..(1337)
; OTHER INFORMATION: Prod
US-10-286-993-1
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Best Local S
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Pred. No. 1.8e-51;
0; Mismatches 263;
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RESULT 12
US-10-213-990-64
US-10-213-990-64
Sequence 64, Application US/10213990
Dublication US20030082595A1
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; ORGANISM: Aspergillus
US-10-213-990-67
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Buskey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 410; Conserv
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SEQ ID NO 67
LENGTH: 739
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Pred. No. 2.6e-49;
0; Mismatches 248;
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                                                  FUMIGATUS
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; CURRENT FILING DATE: 20
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 64
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-64
Sequence 71, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF APPLICANT: APPLICANT: ROEMER, TERRY
TITLE OF INVENTION: ENZYMES AND METHORS.
                                                                                                                                     RESULT 13
US-10-213-990-71
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Pred. No. 8.7e-47;
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   OF ASPERGILLUS
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APPLICANT: Bauer, Michael
APPLICANT: Bedford, Michael
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: Microbially Expressed X;
TITLE OF INVENTION: Uses
FILE REFERENCE: 70357WODCT
CURRENT APPLICATION NUMBER: US/11/018,645
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: 60/531,404
                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-11-018-645-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(942)
US-10-213-990-71
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CURRENT APPLICATION NUMBER: US/10/213,
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 71
LENGTH: 942
                                                                                                                                                                                                                                                                               Sequence 21, Application US/11018645 Publication No. US20050208178A1 GENERAL INFORMATION:
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nes 340; Conserv
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Pred. No. 9.4e-42;
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Sequence 70, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
ITILE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-99
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
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US-10-213-990-70
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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: XylalE
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(978)
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327;
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                                                                                                                                                                                                                                                                                                                                                   GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                  TCGAAGCGCGTGGGCGCACCATCACCATCGCCAACCATTTCAACGCCTGGGCCACGCTG
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                                                                                                                                                                                                                                                                                                                                GGCATGAA---CCTGGGCCAGCACAACTACCAGGTCATGGCCACCGAGGGTTACCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĠTGAACCAGCCATCCATCATCGGCAACGCCACGTTCTACCAGTACTGGAGCGTGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGC
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                                                                     FUMIGATUS ENCODING INDUSTRIAL
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; NUMBER OF SEQ ID NOS: 7; SOFTWARE: FASTSEQ for Wi SEQ ID NO 70; LENGTH: 1002; TYPE: DNA FORGANISM: Aspergillus US-10-213-990-70
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Matches 249; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        CTAGTGACATTACCTTCTCTGGCAGCTTCAATCCTTCCGGAAATGCTTACCTGTCCGTGT
                     CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
                                                                               ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA 622
                                                                                                                                                 ACTGGTCGGTCCGCCAGGACAAGCGCACCAGCCGGTACCGTCCAGACGGGCTGCCACTTCG
                                                                                                                                                                                                                                                                                      ATCCTTCCTGCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGAC
                                                                                                                                                                                                                                                                                                                          ATGGATGGACTACCAACCCCCTAGTCGAATACTACATCCTCGAGAACTATGGCAGTTACA 448
                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCT
CTGAGGGATATGAGAGCAGCGGTACCTCGACCATCACTGT
                                                              AGGCCTGGGCTAGTCTGGGGATGAA----CCTGGGTACCCATAACTATCAGATTGTTTCCA
                                                                                                                              ACTGGTCCATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACCGCGAATCACTTCA
                                                                                                                                                                                             TCTATGAGCACCAACAGGTCAACCAGCCTTCGATCGTCGGCACGGCCACCTTCAACCAAT
                                                                                                                                                                                                                 TCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCCTTCGACCAAT
                                                                                                                                                                                                                                                             ATCCTGGCTCGGGCATGACGCACAAGGGCACCGTCACCAGCGATGGATCCACCTACGACA 508
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Pred. No. 5.6e-36;
0; Mismatches 148;
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Search completed: February Job time: 703.684 secs 11, 2006, 23:51:28

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Maximum DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*

10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*

11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*

12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
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675
1 ATGGTCGGCTTTACCCCCCT
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                     Maximum Match 100%
Listing first 45 summaries
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US-11-108-163B-2

US-10-517-939-155

US-10-517-939-199

US-10-517-939-259

US-10-517-939-271

US-10-517-939-177

US-10-517-939-183

US-10-517-939-183

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US-10-517-939-231
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Sequence 9, Appli
Sequence 231, App
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Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 255, App
Sequence 217, App
Sequence 221, App
Sequence 217, App
Sequence 2183, App
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Sequence 213, App
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Sequence 223, App
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ALIGNMENTS

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.0 1047 7 .0 1029 7 .9 1086 7 .0 108	.0 1077 7 US-10-517-939-181 Sequence .0 1029 7 US-10-517-939-161 Sequence .0 1029 7 US-10-517-939-217 Sequence .0 1029 7 US-10-517-939-227 Sequence .0 1747 7 US-10-517-939-227 Sequence .1 1695 7 US-10-517-939-167 Sequence .2 1086 7 US-10-517-939-167 Sequence .3 1086 7 US-10-517-939-207 Sequence .4 1695 7 US-10-517-939-153 Sequence .5 1086 7 US-10-517-939-169 Sequence .6 133 7 US-10-517-939-169 Sequence .7 1086 7 US-10-517-939-189 Sequence .8 1068 7 US-10-517-939-163 Sequence .8 1068 7 US-10-517-939-163 Sequence .9 1068 7 US-10-517-939-163 Sequence .1 1088 7 US-10-517-939-171 Sequence .2 1020 7 US-10-517-939-171 Sequence .3 1088 7 US-10-517-939-157 Sequence .4 1053 7 US-10-517-939-157 Sequence .5 1083 7 US-10-517-939-157 Sequence .5 1084 7 US-10-517-939-157 Sequence .5 1085 7 US-10-517-939-369 Sequence .5 1085 7 US-10-517-939-369 Sequence	89.8	90.2	91	91	91.4	91.4	91.6	91.8	93.4	94.2	106.8	107.2	108.4	109.2	114.8	116.4	118	119.2	124	127.8	128	131.2	141.8
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7 US-10-517-939-181 7 US-10-517-939-219 7 US-10-517-939-227 7 US-10-517-939-227 7 US-11-214-413-31 1 US-10-517-939-167 1 US-10-517-939-211 7 US-10-517-939-205 1 US-10-517-939-205 7 US-10-517-939-197 7 US-10-517-939-197 7 US-10-517-939-189 1 US-10-517-939-163 3 US-10-517-939-367 7 US-10-517-939-367 9 US-10-517-939-367 1 US-10-517-939-353 7 US-10-517-939-353 8 US-10-517-939-353 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367 9 US-10-517-939-367	Sequence	1077	570	1053	645	1983	678	1338	570	1068	570	555	636	633	1020	1068	1086	669	642	1695	747	1029	1047	1077
US-10-517-939-181 US-10-517-939-219 US-10-517-939-227 US-10-517-939-227 US-10-517-939-217 US-11-517-939-167 US-10-517-939-153 US-10-517-939-153 US-10-517-939-251 US-10-517-939-251 US-10-517-939-251 US-10-517-939-163 US-10-517-939-367 US-10-517-939-367	Sequence	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	11	7	7	7	7	7
		US-10-517-939-369	US-10-517-939-375	US-10-517-939-191	US-10-517-939-157	US-10-517-939-353	US-10-517-939-171	US-10-517-939-367	US-10-517-939-377	US-10-517-939-163	US-10-517-939-189	US-10-517-939-251	US-10-517-939-197	US-10-517-939-207	US-10-517-939-153	US-10-517-939-205	US-10-517-939-211	US-10-517-939-167	US-11-214-413-31	US-10-517-939-317	US-10-517-939-227	US-10-517-939-219	US-10-517-939-161	US-10-517-939-181

Sequence 9, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION: APPLICANT: Danisco A/S APPLICANT: Sibbesen, Ole APPLICANT: Sibbesen, Ole APPLICANT: Sibbesen, Ole APPLICANT: Sibbesen, Ole CURRENT SIBBERGE: 674509-2046 FILE REFERENCE: 674509-2046 CURRENT APPLICATION NUMBER: US/11/170,653 CURRENT FILING DATE: 2005-06-23 PRIOR APPLICATION NUMBER: US/10/237,386 PRIOR FILING DATE: 2002-09-09 PRIOR APPLICATION NUMBER: PCT/IB01/00426 PRIOR FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: GB 0005585.5 PRIOR APPLICATION NUMBER: GB 0015751.1 밁 5 문 5 В S US-11-170-653-9 SOPTWARE: PatentIn version 3.0 SEQ ID NO 9 LENGTH: 588 TYPE: DNA ORGANISM: Thermomyces lanuginosus Query Match Best Local Similarity Matches 214 GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATC 154 GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA 582; 64 94 CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC 4 CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC GGTGGAGCGCAGGCCACGTACACCCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA Conservative 86.2%; Score 582; DB 11; 1 100.0%; Pred. No. 4.7e-156; tive 0; Mismatches 0; Length 588; Indels 0, Gaps 183 273 123 213 63 0

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; SEQ ID NO 231
; LENGTH; 1008
; TYPE: DNA
; ORGANISM: Bacteria
US-10-517-939-231
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
ITITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENG
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-517-939-231
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Best Local S
Matches 376
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APPLICANT: Callen, Walte
APPLICANT: Healey, Shauu
APPLICANT: Hazlewood, Ge
APPLICANT: Blum, David
APPLICANT: Bsteghlalian,
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193
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                                                            133 GTCÁCGACCAACCAGGAGGGCACCAÁCAACGGCTÁCTÁCTÁCTCGTTCTGGÁCCGÁCAGC 192
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Healey, Shaun
Hazlewood, Geoff
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 CAGGGCACCGTCTCCATGAACATGGGCTCCGGCGGTCAGTACAGCACCTCGTGGCGCAAC
                          GGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGAT
                                                                                                                          GTCGCGCTGGCGCGCTCGCCGCGCGCGATGCTGCCGGGCACCGCCCAGGCCGACACGGTC
                                                                                                                                                       GCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGAATGCCACGGAGCTCGAAAAGCGACAG
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o. US20060003433A1
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                   29.8%;
59.9%;
                                                                                                                                                                                      0,
                                                                                                                                                                                      Score 201.2; DB 7;
Pred. No. 1.1e-47;
0; Mismatches 243;
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                                                                                                                                                                                                                    Length 1008;
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 252
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Sequence 1, Application US/11108163B
Publication No. US20060014247A1
GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Regerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Kallio, Jarno
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                                                                                                                                       TYPE: DNA
OTHER INFORMATION: Nf xyn11A nucleotide sequence (AJ508952), the coding region
OTHER INFORMATION: from nt 303 to nt 1337
US-11-108-163B-1
                                                                                                                                                                                                                                                          APPLICANT: Summinen, Pirkko

APPLICANT: Summinen, Pirkko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR FILING DATE: 2005-04-16

NUMBER OF SEQ ID NOS: 25

SOPTWARE: PatentIn version 3.3

SEQ ID NO 1

LENGTH. 1375
                                                             Query Match
Best Local Similarity
Matches 396; Conser
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                                                                                                                                                                                                                                                   LENGTH: 1375
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Kallio, Jarno
Puranen, Terhi
Lantto, Raij
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   TCGGCCTCCGGCGCATCGTCACCAGTGCCTTCGCCCTGGCACTCGCCATCGCCGGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAGCGGCAGCTCCAGCATCAACGTCG
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                                 TCGGCTTTACCCCCGTTGCCCTTGCCGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGG
                                                                                     29.1%;
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                                                                    Score 196.2; DB 11; Length 1375;
Pred. No. 3.1e-46;
D; Mismatches 263; Indels 12;
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Example

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APPLICANT: Puranen, Terhi
APPLICANT: Lentto, Raij
APPLICANT: Lentto, Raij
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
TITLE OP INVENTION: Method and DNA Constructs for Increasing the Production Level of
TITLE OP INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOPTWARE: Patentin version 3.3
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 663
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-11-100-163B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/11108163B Publication No. US20060014247A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Rici
APPLICANT: Kallio, Jarno
ORGANISM: Nonomuraea flexuosa FEATURE: OTHER INFORMATION: am24*, lik
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                                                                                                                                                                                                                                                                                                                                        Fagerstrom, Richard
Kallio, Jarno
like am24 but 9 codons are changed in
the sequence like
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Leskinen, Sanna

--LICANT: Pagerstrom, Richard

APPLICANT: Kallio, Jarno

APPLICANT: Bourinen, Terhi

APPLICANT: Duranen, Terhi

APPLICANT: Sominen, Pirko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION UNMBER: 08/562,692

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.3

SEQ ID NO 4

LENGTH: 906
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Best Local Similarity
Matches 356; Conserv
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Pred. No. 2.
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TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENTITLE OF INVENTION: AND METHODS FOR MAKING ANI PILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
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Best Local S
Matches 356
                                                                                                                                                          APPLICANT: Steer, Brian
APPLICANT: Callen, Waltd
APPLICANT: Healey, Shau
APPLICANT: Hazlewood, G
APPLICANT: Wu, Di
                                                                                                                                                                                                                               Sequence 225, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                APPLICANT:
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Esteghlalian, Alireza
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Healey, Shaun
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5. US20060003433A1
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RESULT 7
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SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 225

LENGTH: 1059

TYPE: DNA

ORGANISM: Unknown

FEATURE:
                                                                                                                                                                                             Sequence 3, Application US/11108163B Publication No. US20060014247A1 GENERAL INFORMATION:
APPLICANT: PAloheimo, Marja APPLICANT: Mantyla, Arja APPLICANT: Leskinen, Sanna
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Best Local (
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APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                      Fagerstrom, Richard
Kallio, Jarno
Puranen, Terhi
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Pred. No. 2e-43;
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PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 3
LENGTH: 663
TYPE: DNA
ORGANISM: Nonomuraea flexuosa
FEATURE:
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US-11-108-163B-2
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                                                                                                                                                                                 Sequence 2, Application US/11108163B Publication No. US20060014247A1 GENERAL INFORMATION:
APPLICANT: Palbheimo, Marja
APPLICANT: Leskinen, Sanna
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Kallio, Jarno
APPLICANT: Puranen, Terhi
APPLICANT: Buominen, Firko
APPLICANT: Suominen, Pirko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
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Best Local &
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Similarity 61.5%;
54; Conservative
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Pred. No. 2e-4:
0; Mismatches
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CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 906
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Best Local Similarity
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ORGANISM: Nonomuraea flexuosa
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OTHER INFORMATION:
OTHER INFORMATION:
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                       AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGC
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                                                                             GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
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Pred. No. 2.2e-43;
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RESULT 9
US-10-517-939-165
Sequence 165, Application US/10517939
Sequence 165, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Hu, Di
APPLICANT: Blum, David
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FITLE OF INVENTION: AND METHODS FOR MAKING
FILE REPERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 165
LENGTH: 1047
TYPE: DNA
Sequence 199, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
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US-10-517-939-199
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OTHER INFORMATION: Obtained from
-10-517-939-165
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Local Similarity 60.6%;
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Pred. No. 4.4e-43;
0; Mismatches 215;
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APPLICANT: Blum, David
APPLICANT: Este9hlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENG
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: 60/889,299
PRIOR A
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Best Local
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  CCGAGGGCTACCAGAGCAGCGGCAGCTCCGACATCACGGT
                                                CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                                       ATGCCTGGGCCAGCCTCGGCATGAA---
                                                                                                                                                        <u>ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA</u>
                                                                                                                                                                                                              ACTGGAGCGTGCGGCAGTCGAAGCGCACCGGCGGCACCATCACCACGGCCAACCACTTCA
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57.5%;
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Pred. No. 8.1e-39;
0; Mismatches 260
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RESULT 11 US-10-517-939-255 • Sequence 255, Ap

Application US/10517939

GENERAL INFORMATION

Publication No. US20060003433A1

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APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Wu, Di
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Bright METHODS FOR MAKING AND USING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: FCT/US03/19153
PRIOR APPLICATION NUMBER: FCT/US03/19153
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTMARE: FRATSEQ for Windows Version 4.0
SOFTMARE: FRATSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACG
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CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCGCCGGGTGGCCAGGGCTTCATGGGCACGGTGAACACCGACGGCGGCACGTACGACA 505
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                                                                                                                                               ACGCCTGGGCTCGCGCTTGGATGTCAACGGTGACCACTACTACCAGATCGTTGCAA 622
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Pred. No. 8.2e-39;
0; Mismatches 260
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PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR FPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 1041
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Obtained
US-10-517-939-169
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Publication No. US20060003
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walte
; APPLICANT: Healey, Shaun
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US-10-517-939-169
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Best Local Similarity
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APPLICANT: Esteghlalian, Alireza
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
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                                                                                                                                                                                                                                                                                                           307 AGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAG 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGG
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ACGGGCTGCCACTTCGACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGACCACTAC
                                                           GCCACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGAAGCGCGTCGGCGGCACGATCACC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAACTACTTTTCCTTCTGGAAGGACAGCCCGGGTACCGTCAACTTCTGCATGTATGCC 171
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                                                                                                                                                                                                                                              AACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGAC 426
                                                                                                                                                                                                                                                                                       GGCTATCTCACCTTGTACGGATGGACCACGAATCCATTGATCGAGTACTACATCGTCGAC 348
                                                                                                                                                                                                                                                                                                                                                                  CAGACGGGCTCCAACCGCACGGTGACCTACTCC---GGTTCGTTCAATTCGCCCGGCAAT
                                                                                                                                  GGCGGCACCTATGACATCTACCGCACGCAGCGCGTGAACCAGCCTTCCATCATCGGCACC
                                                                                                                                                                       GGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACC 486
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Healey, Shaun
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o. US20060003433A1
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246 231

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APPLICANT: Blum, David
APPLICANT: Bsteghlalian, Alireza
ITITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS EN
ITITLE OF INVENTION: AND METHODS FOR MAXING ANI
PILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 221
TENCTH: 1044
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US-10-517-939-221
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Best Local Sim
Matches 332;
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APPLICANT:
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                                                                                                                                                                                                        CGTTCAACTCGCC---CGGCAACGGCTACCTCACCCTGTACGGGTGGACCACGAATCCGC
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                                                                                                                                                                    ACGGCCAACCACTTCAACGCCTGGGCCACGCTGGGCATGAA---CCTGGGCCAGCACAAC
                              ATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCA 463
                                                                                                                                                                                                                                                                                                                                              CGGTGACCTTCTGCATGTATGCCAACGGCCGCTACACCTCCAACTGGAGCGGCATCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCCAGACCGGCACCAÁCAÁCGGCAÁTTÁTTTTTCATTCTGGÁAAGÁCAACCCGGGCA 148
ACCAGCCTTCCATCATCGGCACCGCGACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGA
                                                                 TGATCGAGTACTACATCGTCGACAGTTGGGGCAGTTATCGACCGCCCGGCGGCCAGGGCT
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Healey, Shaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 165.6; DB 7;
Pred. No. 1.4e-37;
O; Mismatches 234;
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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR RPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177
LENGTH: 1299
TYPE: DNA
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Publication No. US20060003433A1
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 351; Conserv
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APPLICANT:
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APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
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                                                                                              GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCCGCAAC 339
                                                                                                                                                                                                                                                                                                            ACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 159
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                         AACGCCACCÁTGACACTCGGTGCCGGTGGAAACTATTCTTCATCCTGGAACAGCAGCACT 207
                                                                                                                                                                                                                                                                                                                                                                                            TGAA---
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                                                                      TCGGGCAGTTATAGCGCGAGTGGAACCAGCTACCTCGCACTTTACGGCTGGACTCGAAAC
                                                                                                                                           AACAACTGGGTTGGCGGTAAAGGCTGGATGCCGGG---TACTCGGCGCACAGTCACCTAT
                                                                                                                                                                          GGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTT 279
                                                                                                                                                                                                                                                 GCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGC 219
                                                                                                                                                                                                                                                                                    AGCTCAAATGCCACTGGAACCCAGAATGGTTACTACTATTCGTTTTGGAAGGATTCCGGT 147
                                                                                                                                                                                                                                                                                                                                                            GCGATTGCTGCCGCAGCACTAGCGGTGGCGACTGTTCCAATCGCTCATGCGCAAACGCTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCTCCGACATCACCGTGACCGAAGGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%;
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Pred. No. 1.7e-37;
0; Mismatches 266;
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   384
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APPLICANT: Blum, David
APPLICANT: Beteghhalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION. AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION NUMBER: US/10/517,939
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PO-15/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOPTWARE: PASUSEQ for Windows Version 4.0
SEQ ID NO 195
LENGTH: 1044
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US-10-517-939-195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 195, Application US/10517939 Publication No. US20060003433A1
                                                                                                                                                                                                                                                                                                                                                             Query Match 23.8%;
Best Local Similarity 59.0%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steer, Brian
APPLICANT: Callen, Walte
APPLICANT: Healey, Shalte
APPLICANT: Hazlewood, Ge
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                          277
                                                                               295
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                                                                                                                                                                                                 157 TGCATGTACTCCGGCGGTCGCTACACGTCGAGCTGGAGCGGCATCAACAACTGGGTCGGC 216
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355 TACATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACT 414
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                                                                                                                                               GGAAAGGGCTGGAACCCCGGCCTGAACGCCAAGAGCCCATCCACTTTGAGGGTGTTTACCAG
                                                                                                                                                                                                                                                                                                                       GGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTAC 174
                                                                                                                                                                                                                                           ACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGT 234
                                                                                                                                                                                                                                                                                   GGCACCAACAACGGCTTCTATTATTCCTTCTGGAAAGACAGTCCGGGTTCAGTGAATTTC
                                     CCG----GGCAATGGCTACCTCGCGCTCTACGGATGGACCACCAATCCACTCGTCGAGTAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Callen, Walter
Healey, Shaun
Hazlewood, Geoff
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                                                                                                                                                                                                                                                                                                                                                             Score 160.8; DB 7;
Pred. No. 3.3e-36;
0; Mismatches 222;
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                                                                       AACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCT
                                                                                                                               AGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCCGCTGGTTTGAATGTC 591
GACCTCACCGTGAGCGAAGGCAGC
                         CGCATCACCGTTGCTGACGTGGGC
                                                                                                                GGCGGAACCATCACCACCGGCAACCACTTCGATGGCTGGGCGAGCTACGGCATGAA---C
                                                                                                                                                                       CTGGGAACTCACAACTACCAGATCCTGGCGACCGAGGGTTATCAAAGCAGCGGCAGCTCG 630
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Search completed: February 11, 2006, 22:06:17 Job time : 217.772 secs



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                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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                                                                                                                                                                                                             Post-processing:
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DB seq length: 2000000000
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1238
1 MVGFTPVALAALAA
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                                                              A_Geneseq_21:*
: geneseqp1980s:*
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              geneseqp2003as:*
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                                                                                                                                                                                                                                                                                                                          439378781 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult

Query

24	23	22	21	20	19	18	17	16	15	14	13	12	H	10	9	8	7	6	v	4	w	N	ب	No.
663	671	678.5	681.5	684.5	684.5	685.5	688.5	688.5	689.5	806.5	806.5	806.5	965	965	965	1083	1083	1083	1088	1238	1238	1238	1238	Score
53.6	•	54.8	•	•		55.4	55.6	55.6		65.1	65.1	65.1	77.9	77.9	•	87.5		87.5	87.9	100.0	•	100.0	100.0	Match
197	234	261	221	223	223	223	227	227	227	221	221	221	194	194	194	194	194	194	194	225	225	225	225	Length
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AAW60736	ABB80186	AAW18115	ABB80185	AAW67567	AAR47122	AAW57422	AAR78231	AAR75421	AEB00301	ADI66756	AAO18654	AAB48548	ADI66750	AA018648	AAB48542	ADI66751	AA018649	AAB48543	AAE18456	AEB00305	ABR63119	AAW05187	AAW01112	ID
Aaw60736 Xylanase	Abb80186 A. fumiga	Aaw18115 Chaetomiu	Abb80185 A. fumiga	Aaw67567 T. reesei	Aar47122 pI 9.0 en	Aaw57422 Amino aci	Aar78231 Humicola	Aar75421 Humicola	Aeb00301 Xylanase	Adi66756 C. carbon	Aaol8654 C carbonu	Aab48548 Cochliobo	Adi66750 P. variot	Aao18648 P variot:	Aab48542 Paecilomy	Adi66751 T. lanugi	Aaol8649 T lanugin	Aab48543 Thermomyc		-	Abr63119 Thermomyc	Aaw05187 Endo-1,4-	ġ.	Description

Aeb47001		19(51.7	640.5	<u>4</u> 5
Aeb47004	0 5 AEB47004	19(51.7	640.5	44
Aao30294		190	52.0	643.5	43
Aao30293		190		643.5	42
Aao30283		190	52.0	643.5	41
Aao30286	0 7 AAO30286	190	52.0	643.5	40
Aao30284 Trichoder		19(643.5	39
Aao30285		190	52.0	643.5	38
Aeb47006		19(52.1	644.5	37
Aae18494 Trichoder		19(52.1	644.5	36
Aae18496		19(52.1	644.5	35
Aeb47005 Thermophi		19(52.2	646.5	34
Aae18492 Trichoder		19(52.2	646.5	33
Aao30297 Trichoder		19	52.3	647.5	32
Aao30298 Trichoder		19(52.3	647.5	31
Aaw18116 Chaetomiu		23	53.5	662.5	30
Adi66745 S.		19		663	29
Aae18445 Schizophy		19.		663	28
Aao18643 S		19	ũ	663	27
Aab48537 Schizophy		19.	53.6	663	26
Aay98068 S.		19	w	663	25

ALIGNMENTS

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RESULT 1
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ID AAWO
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant cell wall; growth
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01-AUG-1996.

26-JAN-1996; 96WO-DK000046

(NOVO) NOVO-NORDISK AS

26-JAN-1995;

95DK-00000094.

Hansen PK, Wagner P, Muellertz A, Клар H,

N-PSDB; AAT40742. WPI; 1996-454790/45.

Fungal xylanase prepns. for use as animal feed additives -construct for producing recombinant Thermomyces xylanase. and DNA

Claim 5; Page 45-46; 69pp; English.

This sequence represents the xylanase from Thermomyces lanuginosus strain DSM 4109. This xylanase, and xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssochlamus or Paecilomyces strains can be used in the monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermomyces xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed conversion

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                      lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pys82.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose- oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endo-1,4-beta-D-xylanase; xylanase;
Humicola lanuginosa; bread; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endo-1,4-beta-D-xylanase
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22-FEB-1997
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                                                                                                                                                                                                                                                                                                        The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a bread-
                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 31-32; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bread improving additive contg. xylanase from Thermomyces - alpha-amylase, increases volume, improves anti-staling prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jorgensen OB,
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                  The present sequence is the protein sequence of a thermostable xylanase of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm) of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, bytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soya, wheat, barley, oats and/or rye
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                                                                                                                                                                                                                                                                                                                   Composition useful as an animal feed additive comprises at least two thermostable enzymes selected from endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase
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                                                                                                         The invention relates to a process for preparing a mash (A) (having enhanced filterability and/or improved extract yield after filtration) which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration step in brewing process. The present sequence represents a xylanase used in the mashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of a mash (having enhanced filterability and/or improved extract yield after filtration) comprises preparing a mash in the presence of enzyme activities comprising xylanase of GH family 10 and presence of enzyme activities comprising xylanase of GH family 10 and presence of enzyme activities comprising xylanase of GH family 10 and presence of enzyme activities comprising xylanase of GH family 10 and presence of enzyme activities comprising xylanase of GH family 10 and 
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Sequence 225

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QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91

Query Match Best Local Similarity Matches 194; Conserv

Conservative

<u>.</u>

Mismatches

100.0%;

Score 1088; DB 5; Pred. No. 1.7e-94;

Length 194; Indels

0,

Gaps

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87.9%;

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Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                         The present invention relates to a modified xylanase exhibiting increased thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to
   Sequence 194 AA;
                                                                                                                                                                                                                              Modified xylanase exhibiting increased thermostability alkalophilicity useful for industrial processing e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dind
                              corresponding native xylanase. The present sequence is lanuginosus xylanase, Xyn
                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                              WPI; 2002-171435/22.
                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001; 2001WO-CA000769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE18456 standard;
                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2000; 2000US-0213803P
                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200192487-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified xylanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermomyces lanuginosus xylanase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manufacture; poultry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
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                                                                                                                                                                                   Page 83-84; 109pp;
                                                                                                                                                                                                                                                                                                                                          RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thermostability; alkalophilicity; industrial process; poultry; swine feed; enzyme; Xyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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Pred. No. 1.3e-108;
                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                    occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bleaching
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 16L; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-679800/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bentzien JM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermomyces lanuginosus xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFEGVYQPNGNSYLAVYGWTKNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 151
                                                                                                                                                                                                                                                                                                                                                       194
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                                    FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
      FEGVYQPNGNSYLAVYGWTRNPLVEYY I VENFGTYDPSSGATDLGTVECDGS I YRLGKTT
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                                                                                                                                                                                                                               87.5%; So ilarity 100.0%; I Conservative 0;
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                                                                                                                                                                                                                               Score 1083; DB 3;
Pred. No. 5.1e-94;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Length 194;
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                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                               identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
starch extraction; food thickener; animal food additive; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2002
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                                                                                                                                                                                                                                              Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 16L; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XENC-) XENCOR INC
                                                                                                                                                      Local
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                                                                                                                     193;
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                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 212
                                                       TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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                                                                                                                     Conservative
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                                                                                                                                                      87.5%; Score 1083; DB 5; 100.0%; Pred. No. 5.1e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, useful in bleaching process of pulp industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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FEGVYOPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT

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RESULT 8
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                                                                                                                                                                                                                                                                                                                           The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADJ66730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADJ66738. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, or 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species
                                                                                                                        Query Match
Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI66751,
                                                                                                                                                                                                                                                Sequence 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 24; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-118575/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper industry; food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T. lanuginosus xylanase
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                                                                                                                                                                                                                                                                                                                 included for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alkali treatment.
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                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGYARITVADVG
                                TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAIH
                                                                                                                    87.5%; Score 1083; DB 8; larity 100.0%; Pred. No. 5.1e-94; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              comparison.
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99US-0138156P.
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                                                                                                                                                                               Length 194;
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RESULT 9
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XX AAB4
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XW Bact
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97 identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-679800/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
                                   153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
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                                                                                                                                                                                                    N
RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF
                                                                                  194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                                                                                                                    TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                      TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 16K; 114pp; English.
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87.6%;
                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                        Score 965; DB 3;
Pred. No. 7.5e-83;
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                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                     alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO18648 standard; protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P variotii xylanase
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 16K; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel xylanase activity protein, useful in bleaching process of pulp in food and animal feed industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-608200/65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-2000; 2000US-00710050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2002
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62
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                                      FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152
   FTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQST
                                                                                                                       TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH
                                                                                                                                                    TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahiyat
                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                              77.9%;
87.6%;
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                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                           Score 965; DB Pred. No. 7.5e 11; Mismatches
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                                                                                                                                                                                                                                                                              DB 5;
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93

Matches

169;

Conservative

33 N

TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH

FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152 TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH Query Match Best Local Similarity

77.9%; Score 965; DB 8; Length 194; 87.6%; Pred. No. 7.5e-83;

Mismatches

Indels

0,

Gaps

61

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RESULT 11
AD166720
ID AD166
XX
XX AD166
XX
XX AD166
XX
XX Pale
DT 22-AI
XX Xylar
XX Xylar
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                                                                                         The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The nonnaturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66730. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, 64, 79, 105 protein in the non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper industry; food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. variotii xylanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-2004
Sequence 194 AA;
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07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hot alkali treatment.
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                                                                      for comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 23; 84pp; English.
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99US-0138156P.
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                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 16Q; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial, Bacillus circulans; xylanase; xylanase activity; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochliobolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (XENC-) XENCOR
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                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                         LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                VENFGTYDDSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
                                                                                                                                                                                                                                                                          MVGFTPVALAALAATGALAFPAGNATELEKROTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                                               GAGGSYSVSWGSGGNL
                                                                                                                                                                                                                       MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGYARITVADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGINVNGDHYYQIVATEGYF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agent.
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbonum xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                        65.1%;
67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
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                                                                                                                                                                                                                                                                                                                              Score 806.5; DB
Pred. No. 9e-68;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 AA
                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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121

VENFGTYDPSSGATDLGTVECDGSIXRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT

GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNSYLAVYGWTRNPLVEYYV LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI

118 120 59

MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN

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                                                Query Match
Best Local S
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                                                                                                                          alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                               The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid community (XA)
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                              activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where protein has been modified to exhibit enhanced thermophilicity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
starch extraction; food thickener; animal food additive; mutant; mutain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cochliobolus carbonum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C carbonum xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA018654;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-608200/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-2000; 2000US-00710050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2001; 2001WO-US048018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                    150;
                                                    Similarity
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   MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMMKTHFDAWASKGMNL-GQHYYQIVATEGYFSTGNAQITV
                                                                                                                                                                                                                                                                                                                                                                                              Fig 16Q;
                                    Conservative
                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahiyat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 221 AA.
                                                  65.1%; Score 806.5; DB 67.9%; Pred. No. 9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                              121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, useful in bleaching process of pulp industry, has enhanced thermostability and
                                    26;
                                    Mismatches
                                    42;
                                                                 5
                                    Indels
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 59, or 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper industry; food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. carbonum xylanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI66756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-2000; 2000US-00570856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                             Sequence 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a mutant xylanase activity (XA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 29; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-118575/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentzien J, Dahiyat
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                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNMKTHFDAWASKGMNL-GOHYYQIVATEGYFSTGNAQITV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS 178
                                      LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNSYLAVYGWTRNPLVEYYV
                                                                                                                          MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN
                                                                                                                                                                                 MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (paper) pulp, and in the food
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                                                                                                                                                                                                                                                                                                                                                                                                                                       comparison.
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99US-0138156P.
                                                                                                                                                                                                                                                                                   65.1%;
67.9%;
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                                                                                                                                                                                                                                                                                   Score 806.5; DB Pred. No. 9e-68;
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                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration step in brewing process. The present sequence represents a xylanase used in the mashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of a mash (having enhanced filterability and/or improved extract yield after filtration) comprises preparing a mash in the presence of enzyme activities comprising xylanase of GH family 10 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB00301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a process for preparing a mash (A) (having enhanced filterability and/or improved extract yield after filtration) which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2003; 2003DK-00001895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-2004; 2004WO-DK000880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2005059084-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylanase SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB00301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 11; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-458778/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Festersen RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             process of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                           56
                                                                                                                                                                                       ш
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                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
                                                               VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGNGYLAVYGWTRNPL
                                                                                                                                                                                                                          MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS 178
      VEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
                                                                                                     ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL
                                                                                                                                                                                    MVSLKSVLAAATAVSSATAAPFDFVPRDNSTALQARQVTPNAEGWHNGYFYSWWSDGGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNMKTHFDAWASKGMNL-GQHYYQIVATEGYFSTGNAQITV
                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to obtain wort.
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viksoe-Nielsen A,
                                                                                                                                                                                                                                                                                                         55.7%; Score 689.5; DB 9
55.8%; Pred. No. 1.1e-56;
tive 31; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joergensen CT,
                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Christensen LLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                        227;
                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                              115
                                                                     119
                                                                                                                                                                                          60
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Db 120 VEYYVIESYGTYNPGSQAQYKGTFYTDGDQYDIFVSTRYNQPSIDGTRTF\ Qy 176 RTSGTVQTGCHFDAWARAGIANVNGDHYYQIVATEGYFSSGYARITV 221	Search Job tim	рb	ş	ğ
: : :: NGPSIDGTRIPQOYWSIRKNK 179 GYARITV 221 : : CESDIYV 224	completed: February 10, 2006, 14:54:12 ne : 153.432	180 RVGGSVNMQNHFNAMQQHGMFL-GQHYYQVVATEGYQSSGESDIYV 224	176 RTSGTVQTGCHFDAWARAGLNVNGDHYYQTVATEGYFSSGYARITV 221	: :

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1238
1 MVGFTPVALAALAATGALAF......VATEGYFSSGYARITVADVG 225
                                                                                                                                                                                                                                                                                       283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              February 10, 2006, 14:54:33 ; Search time 27.9236 Seconds (without alignments) 775.285 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                     283416
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	_S	4	ω	N	1	Regult No.
397.5	_	427	452	468.5	469.5	470.5	498	505.5	528	529	540	553	554.5	ın	585.5	599.5	634.5	636.5	636.5	637.5	659	663	667	•	684.5	689	689.5	691.5	Score
32.1	32.3	4	ō	37.8	7	8	40.2	40.8	42.6	42.7	43.6	44.7	44.8	46.3	47.3	48.4	51.3	51.4	μ	51.5	ω	w	w	55.0	55.3	5	55.7	5	Query Match I
228	261	511	354	213	213	213	656	210	661	644	240	240	241	333	335	221	190	190	190	221	232	197	222	225	223	241	227	219	Length I
μ.	_	μ.	۲	س	_	_	_	N	۲	۲	_	μ	N	۲	N	Ŋ	۲	μ	۲	۲	N	۲	N	-	N	N	N	N	BB
WWBSXP	S12745	JQ1935	851779	S01734	S48126	140569	S59631	C83762	859633	140712	JS0591	847512	T37005	JS0590	T50601	JC7307	A44594	A44595	A44593	S57469	JC7577	A44597	839154	S57477	S39883	S71473	843919	S71472	IB
endo-1,4-beta-xyla	-beta	xylanase 1 - fungu	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyla	Description																					

RESULT 2

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
113	115	145	240.5	248	296	299.5	355.5	356	365	371	372	385	388	389.5	390
9.1	9.3	11.7	19.4	20.0	23.9	24.2	28.7	28.8	29.5	30.0	30.0	31.1	31.3	31.5	31.5
40	2817	50	266	809	607	607	802	209	781	954	229	211	211	789	211
N	N	N	μ	N	N	N	N	N	N	μ	N	Н	_	N	N
PQ0202	B97033	A61149	S48865	B53295	S24754	S49528	A36910	JC4909	S51592	S20907	839155	S48229	JC1198	S58235	S49542
															•
endo-1,4-beta-xyla	uncharacterized p	endo-1,4-beta-xyla	endo-1,4-beta-xyla	xylanase (EC 3.2.	endo-1,4-beta-xyla	endoxylanase - r	xylanase, beta(1,	endo-1,4-beta-xyla	XynB precursor -	endo-1,4-beta-xyl	xylanase 2 - fung	endo-1,4-beta-xyla	endo-1,4-beta-xyla	endo-1,4-beta-xyl	endo-1,4-beta-xyla

Qy 178 SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA 222 : : : : : : :	1 58 57 118 116	Query Match 55.9%; Score 691.5; DB 2; Length 219; Best Local Similarity 59.1%; Pred. No. 5.3e-48; Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps Ov 1 MVGFTPVALAALAATGALAFPAGNATELEKROTTPNSEGWHDGYYYSWWSDGGAOAT	A;Introns: 81/2 C;Function: A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homolo C;Keywords: glycosidase; hydrolase; polysaccharide degradation C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;130/Domain: signal sequence #status predicted cSIG> F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <mat <xyl="" domain:="" endo-1,4-beta-xylanase="" f;42-219="" homology=""> F;115,206/Active site: Glu #status predicted</mat>	081000042480; 081680:061000042480; 8808 8208 ; protein 45,82-94,152-160 <yoh> 668: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82;</yoh>	ase genes	nge N.	RESULT 1 S71472 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile	
		219; 9; Gaps 5; SWWSDGGAOAT 57	homology 1 11 <mat></mat>	C:UPI0000175AE	and their expression in Asp	e 09-Jul-2004 N.	racile	endo-i,4-beta-xyla xylanase (EC 3.2.1 endo-1,4-beta-xyla endo-1,4-beta-xyla uncharacterized pr endo-1,4-beta-xyla

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RESULT 3
871473
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
C.Species: Chaetomium gracile
C.Species: Chaetomium gracile
C.Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C.Accession: 871473; 878207
C.Accession: 871473; 878207
C.Accession: 871473; 878207
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Mol. Gen. Genet. 243, 253-260, 1994
A;Title: A novel method for efficient expression cloning
A;Reference number: $43919; MUID:94247364; PMID:8190078
A;Accession: $43919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Pathway: xylan degradation
C; Superfamily: endo-1, 4-beta-xylanase; endo-1, 4-beta-xylanase homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 1-19/Domain: endo-1, 4-beta-xylanase #status predicted <MAT>
F; 20-227/Product: endo-1, 4-beta-xylanase #status predicted <MAT>
F; 448-225/Domain: endo-1, 4-beta-xylanase #status predicted
F; 448-225/Domain: endo-1, 4-beta-xylanase #status predicted
A; Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Not the sequence #status predicted <SIGS
F; 1-30/Domain: signal sequence #status predicted <MAT>
F; 31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 38-44;89-91;153-161 <YOH>
A;Cross-references: UNIPARC:UPI0000175A77;
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Two family G xylanase genes from Chaetomium gracile and A;Reference number: S71472; MUID:96118924; PMID:8595661 A;Accession: S71473
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C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P55334; UNIPARC:UPI00000421A4; EMBL:X76047; NID:g505260; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-227 < DAL>
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                                                                                                                                            A; Introns: 88/2
C; Function:
                                                                                                                                                                                                     A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Yoshino, S.; Oishi, M.; Moriyama, R.; Curr. Genet. 29, 73-80, 1995
                                                                                                                                                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-241 <YOS>
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Species: Humicola insolens
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
;Accession: S43919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;121,212/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                   Cross-references:
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Best Local S
                                                                                                                                                                                                  Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity 55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGNGYLAVYGWTRNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEYYVIESYGTYNPGSQAQYKGTFYTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEYYIVENPGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVGGSVNMQNHFNAWQQHGMPL-GQHYYQVVATEGYQSSGESDIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVSLKSVLAAATAVSSATAAPFDFVPRDNSTALQARQVTPNAEGWHNGYFYSWWSDGGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                      UNIPROT:Q12580; UNIPARC:UPI00000421AB; EMBL:D49851; NID:g1339859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 689.5; 1; Pred. No. 8e-4; 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31,
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                                                                                                                                                                                                                              UNIPARC:UPI0000175A78; UNIPARC:UPI0000175A79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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119

YIVENEGTYDESSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTEDQYWSVRQDKRTS

TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEY

120

61

F;116,207/Active site: Glu #status predicted

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RESULT
S39883
                                                                                                                                                                                          F;20-33/Domain: propeptide #status predicted <PRO>
F;34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT:
F;45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F;71-23/Domain: endo-1,4-beta-xylanase homology <XYL>
F;717,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;110,121/Binding site: substrate (Tyr) #status predicted
F;119,210/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                    A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bon A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase hom C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endo-1,4-beta-xylanase (EC 3.2.1.8)
N;Alternate names: endoxylanase II
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                                                                                                                                                                                                                                                                                                                                                                                              C; Function:
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A; Residues: 1-223 <SAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Cloning, sequencing and enhanced A;Reference number: S39883; MUID:94088442; A;Accession: S39883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멼
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 91/2
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: xln2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 34-43;49-57;121-151;178-191 <SAF>
A;Cross-references: UNIPARC:UPI0000175A7C; UNIPARC:UPI0000175A7D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S39884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q02244;
A;Experimental source: strain QM6a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                    Matches
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Best Local
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                                                                             μ
                                                                             MVGFTPVALAALAATGALAFPAG--NATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVENFGTYNPSTGATRLGSVTTDGSCYDIYRTQRVNQPSIEGTSTFYQFWSVRQNKRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEAGGQYSVTWSGNGNWVGGKGWNPG-SARTINYTANYNPNGNSYLAVYGWTRNPLIEYY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVNMAAHFNAWAAAGLQL-GTHDYQIVATEGYYSSGSATVNV
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                                      TNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY
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                                                                                                                                   55.3%;
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                                                                                                                                 Score 684.5; DB 2;
Pred. No. 2e-47;
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Pred. No. 9.4e-48;
1; Mismatches 55;
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                                                                                                                    Mismatches
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                                                                                                                    61;
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                                                                                                                                                                                                                                                                                                                                             homology
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DIG

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xylanase 1 - fungus (Trichoderma reesei)
C;Species: Trichoderma reesei
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S39154
R;Toerroenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A..
Biotechnology 10, 1461-1465, 1992
A;Title: The two major xylanases from trichoderma reesei: characterization of both A;Reference number: S39154
A;Reference number: S39154
A;Accession: S39154
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <TOE>
A;Cross-references: UNIPROT:P36217; UNIPARC:UPI00000421A9; EMBL:X69573; NID:g39656: C;Genetics:
A;Gene: xyn1
A;Introns: 90/2
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S57477

S57477

sendo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans endo-1,4-beta-xylanase 1

C;Species: Emericella nidulans, Aspergillus nidulans
C;Apte: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S57477

R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A,Description: Expression in Saccharomyces cerevisiae of two xylanase encoding callection: S57477
A;Accession: S57469
A;Accession: S57477
A;Molecule type: DNA
A;Residues: 1-225 <PER>
A;Gross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:g870
C;Genetics:
A;Introns: 93/2
C;Function:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;48-25/Domain: endo-1,4-beta-xylanase | #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ঠ
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Best Local S
Matches 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
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29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDVTYTNGAGGSYTVQWSNVGNFVGGKGWNPG-STRTINYGGSFNPSGNGYLAVYGWTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVSFKSLLVLCCAALGAFATPVGSEDLAAREASLLER--STPSSTGWSNGYYYSFWTDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSVNTANHFNAWAQQGLTL-GTMDYQIVAVEGYFSSGSASITVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.0%; Score 680.5; DB 1; 56.6%; Pred. No. 4.1e-47; Mismatches 57;
                                                                             UNIPARC:UPI00000421A9; EMBL:X69573; NID:g396563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIPARC:UPI0000139073; EMBL:Z49892; NID:g870832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB_1; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                               Harkki,
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                                                                                                                                                                                A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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A; Molecule type: protein
A; Residues: 1-197 <OKU>
A; Cross-references: UNIPAR
A; Experimental source: ATC
C; Function:
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A;Cross-references: UNIPAKL:UFAUT.
A;Cross-references: UNIPAKL:UFAUT.
A;Cross-references: UNIPAKL:UFAUT.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Lamper.
R;Oku, T.; Roy, C.; Watson, D.C.; Wats
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: extracellular protein; glycosidase; hydrolase; pol
F;12-197/Domain: endo-1,4-beta-xylanase homology <XYL>
F;87,184/Active site: Glu #status predicted
F;111-160/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI0000172966
R;Paice, M.G.; Jurasek, L.; Carpenter, M.R.;
Appl. Environ. Microbiol. 36, 802-808, 1978
A;Reference number: A05147; MUID:79102289; PM
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C;Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A44597; S41411; A05147; S38973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-27 < PAI >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A05147; A; Accession: A05147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Identification of a glutamate residue at the active site of xylanase A;Reference number: S41411; MUID:94155888; PMID:7906649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bray, M.R.; Clarke, A.J.
Eur. J. Biochem. 219, 821-827, 1994
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A;Experimental source: strain Delmar ATCC 38548
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submitted to the Protein Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
F;44-222/Domain: endo-1,4-beta-xylanase homology <XYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 83-123 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endo-1,4-beta-xylanase (EC 3.2.1.8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-197 even
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSS
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                                                                                                                                                                                                                                                                     catalyzes the hydrolysis of 1,4-beta-xylosidic
                                                                                                                                                                                                                                                                                                                                                      source: ATCC
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Pred. No. 4.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell, R.; Yaguchi, M.; Jurasek, L.;
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R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morin Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification A;Reference number: JC7577; MUID: 21077500; PMID:11210150
A;Accession: JC7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7577; PC7120
RESULT 9

55746-1,4-beta-xylanase (EC 3

endo-1,4-beta-xylanase (EC 3

N;Alternate names: xylanase :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 100/2
C;Superfamily: endo-1,4-1
C;Keywords: glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-232 <KIM>
A;Cross-references: UNIPROT:Q9HFA4; UNIPARC:UPI0000069976; DDBJ:AB044941
A;Experimental source: strain KBN616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 45-64 < KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
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                                                                                                                                                                                                                   GWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA
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                                                                                                                                 WSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                                                                                                                                      WTDGGGDVTYTNGNGGSYSVQWSNVGNFVGGKGWNPG-SSRAITYSGSFNPSGNGYLAVY
                                                                                                                                                                                                                                                                                                                                                                 MVGFTPVALAALAATGALAFP------AGNATELEK--RQTTPNSEGWHDGYYYSW 48
                                                                                                                                                                                 GWTTDPLIEYYIVESYGTYNPGSGGTYKGQVTSDGGTYNIYTSVRTNAPSIIGTATFTQF
                                                                                                                                                                                                                                                                                        WSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVY
                                                                                                                                                                                                                                                                                                                             MVSFSSILLACSAAIGALATPIEPLADHPNEAFNETAFNDLVGRSTPSSTGYNNGYYYSF
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ycosidase; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                  53.2%; Score 659; DB 2; 54.9%; Pred. No. 2.2e-45;
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                  .2.1.8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity
                      N
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                    Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 232;
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A;Cross-references: UNIPARC:UPI00000493CB
A;Experimental source: strain E58
R;Campbell, R.L.; Rose, D.R.
submitted to the Brookhaven Protein Data Bank,
A;Reference number: A52868; PDB:1XND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endo-1,4-beta-xylanase (EC 3.2.1.8)
N;Alternate names: xylanase
C;Species: Trichoderma harzianum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>F;44-221/Domain: endo-1,4-beta-xylanase homology <XYL>F;117,208/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: endo-1,4-Deta-Xy1anabe; enwo-1,7-vouc
C;Keywords: glycosidase; hydrolase; polysaccharide degi
C;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1995 A;Description: Expression in Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Emericella
C;Date: 10-Oct-1995 #s
C;Accession: S57469
R;Perez-Gonzalez, J.A.
A;Pathway: xylan degradation
(C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F;86,177/Active site: Glu #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase homology
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C; Function:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-221 < PER>
                                                                                                                                                                                                                                                                                                                                                                                                                            R; Yaguchi, M. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description:
                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-190 < YAG>
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: A44593
                                                                                                                                                                            A; Contents:
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                                                                                                                         Description: catalyzes the hydrolysis of 1,4-beta-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Trichoderma harzianum
;Date: 27-Jun-1994 #sequence_revision
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Best Local (
                                                                                                                                                ; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Accession:
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                                                                                                                                                                            annotation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVGFTPVALAALAATGALAFPAGNATELEKR----OTTPNSEGWHDGYYYSWWSDGGAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVSFSSLLLACSAVT---AFAAPSDQSIAERSLSERSTPSSTGTSGGYYYSFWTDGGGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSGSVTTQNHFDAWSQLGMTL-GTHNYQIVAVEGYQSSGSASITVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYYIVESYGDYNPGTAGTHQGTLESDGSTYDIYTATRENAPSIEGTATFTQFWSVRQSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYTNGDGGSYTVEWTKVGNFVGGKGWNPG-SSQTISYSGSFIPSGNGYLSVYGWTQNPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       A44593
                                                                                                                                                                            X-ray crystallography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.0%;
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Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                            Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [validated]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                 March 1994
                                                                                                                                                                                                                                June 1994
                                                                                                                                                                          1.8 angstroms,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungus (Trichoderma harzianum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 15-Sep-2000
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                                                                                                                              bonds in
                                                                                                                                                                               residues 1-46,'A'48-190
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Similarity

51.4%; 60.7%;

Score 636.5; DB 1; Pred. No. 1.1e-43;

Length 190;

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RESULT 12
A44594
endo-1.4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N;Alternate names: xylanase IIA
C;Species: Trichoderma viride
C;Species: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A44594
R;Yaguchi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in A;Pathway: xylan degradation G;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation C;Keywords: endo-1,4-beta-xylanase homology <XYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
A44595
endo-1,4-beta-xylanase (EC 3.2.1.8)
N;Alternate names: xylanase IIB
C;Species: Trichoderma viride
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Cross-references: UNIPROT:Q7M520; UNIPARC:UPI0000172968 C/Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-190 < YAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Yaguchi, M. submitted to the Protein Sequence Database, March 1994
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A;Accession: A44595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          용
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6-127/Cleavage site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -130/Cleavage site:
                                                                                                                                                                                            180
                                                                                                                                                                                                                                 212
                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ORVNOPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NFSGSYNPNGNSYLSIYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                 QRVNQPSIEGTSTFYQYWSVRRTHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY
                                                                                                                                                                                                                                                                                                                                           NFSGTYNPNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                             FSSGYARITVA 222
                                                                                                                                                                                                                                                                                                                                                                               HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 151
                                                                                                                                                                                                                                                                                                                                                                                                                QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSSGYARITVA 222
                                                                                                                                                                                                                                                                                                    TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 211
                                                                                                                                                                                          PSSGSASITVS 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glu-Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.4%; Score 636.5; DB 1 60.2%; Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteinase) #status
proteinase) #status
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A,Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C;Keywords: glycosidase, hydrolase; polysaccharide degradation F;12-190/Domain: endo-1,4-beta-xylanase homology xYIL> F;77,88/Binding site: substrate (Tyr) #status predicted F;86,177/Active site: Glu #status predicted
                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Purification, cha A; Reference number: JC7307 A; Accession: JC7307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp
N;Alternate names: endo-1,3-beta-xylanase; xylanase
C;Species: Penicillium sp.
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                                                                                                                                                                                                                                                                                                          A; Introns: 89/2
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 32-51 < KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9UUQ2; UNIPARC:UPI00000421AD; DDBJ:AB035540 A;Accession: PC7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-221 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya, Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
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                                                                                                                                                                                                                                                                                                                               A;Gene: xynA
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI0000175A85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-190 < YAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A44594
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                                                                                                                                                                                                                                                            ;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
;Keywords: glycoprotein; glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: JC7307; PC7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: A44593
                                                                                                                                                                         Matches
                                                                                                                                                                                                                     Query Match
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                           NLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
                                                                                                                              MVGFTPVALAALAATGALAFPAGNATELEKROTTPNSE-GWHDGYYYSWWSDGGAQATYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRVNQPSIIGTSTFYQYWSVRRTHRSSGSVNTANHENAWAQQGLTL-GTMDYQIVAVEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENPGTYDPSSGATDLGTVECDGSIYRLGKT 151
                                                                                    MKSFIAYLLASVAVTGVMAVPGEYHKRHDKRQTITSSQTGTNNGYYYSFWTNGGGTVQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSSGSASITVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFSGTYNPNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTIGPGTGFNNGYFYSYWNDGHGGVTYTNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization, and molecular cloning
                                                                                                                                                                                         48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                            Score 599.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 634.5; DB 1
Pred. No. 1.6e-43;
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N;Alternate names: xylanase B (;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50601 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50601 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50601 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50601
                                                                                                                                                                                                                                                                                                                                endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans NyAlternate names: xylanase B C;Species: Streptomyces lividans C;Date: 10-Mar-1994 #sequence revision 22-Nov-1996 #text_change 26-Feb-C;Accession: JS0590; PS0239
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JS0590
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                                                                                                                                                                                                                                  C;Species: Streptomyces lividans
C;Date: 10.Mar-1994 #sequence_revision 22-Nov-1996 #text_change C;Date: 10.Mar-1999, P80239
R;Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D. Gene 107, 75-82, 1991
A;Title: Sequences of three genes specifying xylanases in Strept A;Reference number: JS0589; MUID:92077439; PMID:1743521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-335 < RED>
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A; Gene:
                                                                   A; Molecule type: protein A; Residues: 41-71 <SH2>
                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-333 <SHA>
                                          A; Cross-references: UNIPARC: UPI000017296B
                                                                                                               A;Cross-references: UNIPARC:UPI000017296A; GB:M64552
A;Accession: PS0239
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Matches 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVENEGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTEDQYWSVRQDKRTSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THLEGGTYEISWGDGGHLVGGKGWNPGLNARAIHFEGVYQPHGNSYLAVYGWTRNPLVEY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTITTGNHFDAWARAGMPLGNFSYYMIMATEGYOSSGSSSINVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG 225
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Pred. No. 2.4e-39;
24; Mismatches 73;
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C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A;Destription: cylan degradation
A;Pathway: xylan degradation
C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-40/Domain: signal sequence #scatus predicted <SIG>
F;41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F;54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
F;127,217/Active site: Glu #status predicted
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Similarity 51.4%;
                               DAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG 225
                                                                                   RPTGEYK--GTVTSDGGTYDIYKTTRVNKPSVEGTRTEDQYWSVRQSKRTGGTITTGNHF 195
                                                                                                                     DPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHF 187
                                                                                                                                                                      TSWRNTGNFVAGKGWANG-GRRTVQYSGSFNPSGNAYLALYGWTSNPLVEYYIVDNWGTY
                                                                                                                                                                                                            ISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTY 127
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DAWARAGMPLGNFSYYMIMATEGYQSSGTSSINVGGTG
                                                                                                                                                                                                                                                            AWAVALARSPLMLP---GTAQADTVVTTNQEGTNNGYYYSFWTDSQGTVSMNMGSGGQYS 78
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Score 573; DB 1; 1
Pred. No. 2.3e-38;
4; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                        Length 333
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Search completed: February 10, 2006, 15:02:20 Job time: 28.9236 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
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http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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        MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348; Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Viswamitra M.A.; Withayathil p.J., Viswamitra
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PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.

3D-structure; Acetylation; Direct protein se Hydrolase; Xylan degradation.

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Degefu Y., Paulin L., Lubeck P.S.;
Cloning, sequencing and expression of a xy
pathogen Helminthosporium turcicum Pass.";
Eur. J. Plant Pathol. 107:457-465(2001).
RMBL; AJ238895; CAB52417.1; -; Genomic_DNA
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InterPro; IPR001137; Glyco_hydro_11.
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Best Local S
Matches 153
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GO; GO:00045493; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PP00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
SIGNAL 1 19 Potential.
CHAIN 20 227 xylanase.
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.

STRAIN=Race 1 / Isolate SB111;

MEDLINE=94003417; PubMed=8400376;

Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;

"Cloning and targeted gene disruption of XYI1, a beta gene from the maize pathogen Cochliobolus carbonum.";

Mol. Plant Microbe Interact. 6:467-473(1993).
                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8)
beta-D-xylan xylanohydrolase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                       XYN1_CO
                                                                                                                                                                                                                                                                                                      Cochliobolus carbonum (Bipolaris zeicola).
Bukaryota, Fungi, Ascomycota, Pezizomycotina,
Pleosporales, Pleosporacese, Cochliobolus.
                                                                                                Holden F.R., Walton J.D.;
"Xylanases from the fungal maize pathogen Cc
Physiol. Mol. Plant Pathol. 40:39-47(1992).
-I- FUNCTION: Major xylan-degrading enzyme.
hydrolysis of arabinoxylan, the major cc
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                                                                              Name=XYL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                PARTIAL
PTM: The N-terminus is blocked. SIMILARITY: Belongs to the glycfamily.
                                    linkages in xylans.
PATHWAY: Xylan degradation.
SUBCELLULAR LOCATION: Secreted.
                                                                         CATALYTIC ACTIVITY: Endohydrolysis
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Pred. No. 5.3e-61;
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             glycosyl
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Best Local S
Matches 150
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01-JUN-2001
01-OCT-2003
NUCLEOTIDE SEQUENCE.

MEDILINE=21654148; PubMed=11795847; DOI=10.1007/800294-001-0260-0;

Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;

"Molecular characterization of a novel endo-beta-1.4-xylanase genuter of the vascular wilt fungus fusarium oxysporum.";

Curr. Genet. 40:268-275(2001).

RMBL; AF246830; AAK27974.1; -; Genomic_DNA.

RMSB; O43097; IYNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:00045493; P:xylan catabolism; IEA.
                                                                                                                                                                                                                                                Eularyota; Fungi; Ascomycota; Pezizomycotina; Sordariomy Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.
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CHAIN
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                                                                                                                                                                                                                                     Fusarium oxysporum NCBI_TaxID=59765;
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PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.
Direct protein sequencing; Glycosidase; Hydrolase;
Xylan degradation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00911; GLHYDRLASE11
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Pfam; PF00457; Glyco_hydro_11; 1.
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7562; 31-218.
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Endo-1, 4-beta-xylanase I.
Nucleophile (By similarity).
Proton donor (By similarity).
W -> I (in Ref. 2).
G -> A (in Ref. 2).
S -> W (in Ref. 2).
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Q00263;
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PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; PR05ITE; PS00777; GLYCOSYL_HYDROL_F11_2; Xylan degradation.
                                                                                                                                                             PROSITE; PS00776; GLYCOSYL HYDROL F11 1;
PROSITE; PS00777; GLYCOSYL HYDROL F11 2;
Signal; Xylan degradation.
SIGNAL 1 19
                                                                                                                                                                                                                                                                                      EMBL;
HSSP;
SMR; C
                                                                                                                                                                                                                                                                                                 Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collin "Molecular cloning and DNA sequencing of a xylanase phytopathogenic fungus Ascochyta pisi Lib."; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databa EMBL; Z68891; CAA93120.1; -; Genomic_DNA.

HSSP; 043097; 1YNA.
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                                                                                                                                                                                                          GO; GO:0004553; F:hydrolase activity, hydrolyzing GO; GO:0005975; F:carbohydrate metabolism; IEA. GO; GO:0045493; F:xylan catabolism; IEA. InterPro; IPR001137; Glyco hydro 11. Pfam; PF00457; Glyco hydro 11; 1. PFINTS; PR00911; GIYDOLASEII.
                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                   mitosporic Pezizomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endo-1,4-betaxylanase precursor.
                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=47971;
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ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL
                                                            WVGFTPVALAALAATGALAFPAGN-ATE----LEKROTTPNSEGWHDGYYYSWWSDGGAO
                                      MVSFTSIFTAAVAATGALAVPVTDLATRSLGALTARAGTPSSQGTHNGCFYSWWTDGGAQ
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24010 MW;
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64.9%; Pred. No. 8.4e-58;
tive 30; Mismatches 45
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
NCBI_TaxID=148305;
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Q92245;
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47 COCSA
O13447 COCSA PRELIMINARY;
O13447;
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                                                                                         01-JAN-1998
01-JAN-1998
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                                                                   (TrEMBLrel. 05, (TrEMBLrel. 25,
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_hydro_11; 1.
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Pred. No. 3.9e-53;
9; Mismatches 53
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Name=xy12 Beta-1, 4-xylanase.

Cochliobolus

sativus

(Bipolaris

sorokiniana)

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RESULT IS A CONTROL OF STANKING OF STANKIN
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A Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
A Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
A Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
A Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
A Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
A Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
A Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
A Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
A Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
A David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
A Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
A Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
A Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
A Hizgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
A Hizgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
A Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
A Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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13-SEP-2005 (TrEMBLrel. 31, L.
13-SEP-2005 (TrEMBLrel. 31, L.
13-SEP-2005 (TrEMBLrel. 31, L.
Hypothetical protein.
ORFNames MG08424.4;
Magnaporthe grisea 70-15.
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SA1 MAGGR
Q51SA1, MAGGR PRELIMINARY;
Q51SA1;
13-SEP-2005 (TrembLrel. 31,
13-SEP-2005 (TrembLrel. 31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota;
Sordariomycetes incertae sedis
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=70-15;
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Pleosporales; Ple
NCBI_TaxID=45130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterisation of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGSAQYTMGEGSRYSUTWRNTGNFVGGKGWNPG-TGRVINYGGAFNPQGNGYLAVYGWT
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s; Magnaporthaceae; Magnaporthe.
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                                                                 Hafez N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C preliminary data.

R EMBL; AACU01001255; EAA49509.1; -; Genomic_DNA.

R InterPro; IPR002453; Beta tubulin.

R InterPro; IPR001137; Glyco_hydro_11.

R Pfam; pP60457; Glyco_hydro_11; 1.

R PRINTS; PR00911; GLHYDRLASE11.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

R PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

R PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

R PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 204 AA; 22624 MW; 2396D83ED2B92260 CH
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhu H., Blackmon B.;
Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=70-15;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                          RLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIV
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                                                          ATEGYFSSGYARITV
                                                                                                                            QVAQSTRTNQPSIDGTRTFQQYWSVRQQKRSSGTVDMKKHFDAWASMGMKL-GTHDYQIV
                                                                                                                                                                                                                                                           SARNVTYSANYRPNGNSYLSVYGWTRNPLVEYYVVENFGTYDPSSQASRKGTINVDGATY
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65.1%;
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Pred. No. 9.2e
26; Mismatches
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EMBL/GenBank/DDBJ databases.
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RESULT 10 Q70T28_9PLEO

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RESULT COS50
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Matches 133
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HSSP; P09850; 1BCX.
G0; G0:0004553; F:hydrolase activity, hydrolyzing O-glycosyl .
G0; G0:0005975; P:carbohydrate metabolism; IEA.
G0; G0:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
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"Expression patterns and phylogenetic analysis of (htxyl 1 and htxyl 2) from Helminthosporium turcicu leaf blight of maize.";
                                                                                                                                        Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Xylan degradation. SIGNAL 1 19
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Name=xyl2;
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05-JUL-2004
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Q70T28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=93612;
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  MEDLINE=97055717; PubMed=8900004; Apel-Birkhold P.C., Walton J.D.;
                                                  STRAIN=SB111;
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57.8%; Pred. No. 1.20
tive 30; Mismatches
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Q9HGE1 HUMGT
Q9HGE1 H
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DT Q1-MAR-2
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SEQUENCE
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EMBL; US915; AAC62815.1; Genomic_DNA.

HSSP; Q8J1V6; 1H1A.

G0; G0:000595; F:hydrolase activity, hydrolyzing 0-gl G0; G0:000595; P:carbohydrate metabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

PRINTS; PR00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.
                                                                                                                              PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; Xylan degradation.
SEQUENCE 227 AA; 25615 MW: 991815ADB4
                                                                                                                                                                                                                                         GO; GO:0004553; F:hydrolase activity, hydrolyzing GO; GO:0005975; P:carbohlydrate metabolism; IEA. GO; GO:0045493; F:xylan catabolism; IEA. InterPro; IPR001137; Glyco_hydro_11. Pfam; PF00457; Glyco_hydro_11; 1.
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1 41 Potential.
                                                                                                                                                                                                                                                                                                                                                     Faria F.P., Pocas-Fonseca M.J., Azevedo M.O Submitted (JUN-1999) to the EMBL/GenBank/DD EMBL; AF155594; AAG16891.1; -; Genomic_DNA. HSSP; O43097; IYNA.
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Bukaryota; Fungi; Ascomycota; mitosporic
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    MVGFTPVALAALAATGALA--
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41
231 AA;
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231 X
25576 MW;
                                                              55.98;
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he EMBL/GenBank/DDBJ
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                                              29;
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Last sequence update)
Last annotation update)
                                           Score 692.5;
Pred. No. 3.7e
Pred. Mismatches
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Pred. No. 6.7e-51
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; 237C3D49C4D0E871 CRC64;
                                                                                                                                   991815AD84EB2939 CRC64;
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  -FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ
                                                                  692.5; DB 2
No. 3.7e-50;
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579_9PEZI
501579_9PEZI PRELIMINARY;
Q12579;
Q12579;
G1-SOV-1996 (TremBLrel. 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196; Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.; "Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans."; Curr. Genet. 29:73-80(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=cgxA;
Chaetomium gracile.
Chaetomium gracile.
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.

PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.

Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P36217; 1XYO.
GO; GO:0031176; F:endo-1,4-beta-xylanase activity;
GO; GO:0005975; F:carbohydrate metabolism; IEA.
GO; GO:0045493; F:xylan catabolism; IEA.
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01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Endo-betal,4-xylanase A
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176
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                                                                                                                                                                                                                                                                                                                                                    MVGFTPVALAALAATGALAFPAGNAT----ELEKRQTTPNSEGWHDGYYYSWWSDGGAQAT
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                                                                                             YYIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTRVNQPSIEGTSTFDQFWSVRQNHRS
                                                                                                                           YYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRT 177
                                                                                                                                                                                                                              YTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVE
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                                                                                                                                                                                                                                                                                                      MVSFKAL---LLGAAGALAPPF-NVTQMNELVARAGTPSGTGTNNGYFYSFWTDGGGTVN
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Last annotation updat
3.2.1.8).
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Pred. No. 4.3e-50;
29; Mismatches 54;
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RESULT 15
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PRINTS; PR00911; GLHYDRLASE11.
PROSITE; P800776; GLYCOSYL_HYDROL_F11_1;
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2;
Glycosidase; Hydrolase; Signal; Xylan_deg:
SIGNAL 1 19
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P55334; Q12625;
01-OCT-1996 (Re
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ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X76047; CAA53632.1;
PIR; S43919; S43919.
HSSP; O43097; 1YNA.
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MEDLINE=94247364; PubMed=8190078; DOI=10.1007/BF00301060; Dalboege H., Hansen H.P.H.;

"A novel method for efficient expression cloning of funga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence upo
10-MAY-2005 (Rel. 47, Last annotation u
Endo-1,4-beta-xylanase 1 precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 243:253-260(1994).
-!- CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes.
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NCBI_TaxID=34413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humicola insolens
                                                                                                                                                                                                                                                                           Local
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Buropean Bioinformatics
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PATHWAY: Xylan degradation.
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                                                                                                                                                                                                                             MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ
                                                                                RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
                                                                                                               VBYYVIESYGTYNPGSQAQYKGTFYTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKNK
                                                                                                                                 VBYYIVENPGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
                                                                                                                                                                  VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGNGYLAVYGWTRNPL
                                                                                                                                                                                                               RVGGSVNMQNHFNAWQQHGMPL-GQHYYQVVATEGYQSSGESDIYV
                                                                                                                                                                                       ATYTNIEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL
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Pred. No. 6.7e-50;
1; Mismatches 62;
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R EMBL; D49851; BAA08650.1; -; Genomic_DNA.

R PIR; S71473; S71473.

R PIR; G011V6; I11A.

R SMR; Q12580; 31-220.

R GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR001137; Glyco hydro 11.

R PINTS; PR00917; Glyco hydro 11.

R PRINTS; PR00917; GLYCOSYL HYDROL F11 1; 1.

R PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.

Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Endo-betal, 4-xylanase (EC 3.2.1.8).
Name-cysB;
Chaetomium gracile.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomium.
NCBI TaxID-47794;
NCBI TaxID-47794;
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MEDLINE-96118924; PubMed-8595661; DOI=10.1007/BF00313196;
MEDLINE-96118924; PubMed-8595661; DOI=10.1007/BF00313196;
YOshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
"Two family G xylanase genes from Chaetomium gracile and their
expression in Aspergillus nidulans.";
Curr Genet. 29:73-80(1995).
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Search completed: February Job time: 230.148 secs

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1: /cgm2_6/ptodata/1.
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US-08-121-436A-2
US-09-849-242A-2
US-08-044-621D-29
US-08-044-621D-29
US-09-649-242A-2
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APPLICANT: Kullertz, Anette APPLICANT: Knap, Inge Helmer TITLE OF INVENTION: Animal Feed NUMBER OF SEQUENCES: 2

Additives

Wagner, Peter Mullertz, Anette

Hansen,

Peter Kamp

630.5 50.9 190 2 US-09-570-8568-22 628 50.7 225 1 US-08-290-978-8 610.28 50.7 225 1 US-08-290-978-8 610.28 50.7 225 1 US-08-290-978-8 610.28 50.7 225 2 US-09-367-8918-2 50.8 5 47.5 296 2 US-09-110-622-6 588.5 47.5 296 2 US-09-219-277-6 588.5 47.5 296 2 US-09-219-277-6 588.5 47.5 296 2 US-09-219-277-6 588.5 47.4 231 1 US-08-90-5588-6 5971.5 46.2 215 1 US-08-902-6558-6 571.5 46.2 215 1 US-08-902-6558-6 571.5 46.2 215 1 US-08-902-6558-6 5971.5 46.2 215 1 US-08-902-6558-6 5971.5 46.2 215 1 US-08-902-6558-6 5971.5 46.2 215 1 US-08-902-6558-6 45.7 344 2 US-08-913-695-19 566 45.7 344 2 US-08-90-503-2 566 45.7 344 2 US-08-90-503-2	.5 50.9 190 2 US-09-570-856B-22 Sequence 59.7 225 1 US-08-290-979A-8 Sequence 59.7 225 2 US-09-462-245-2 Sequence 59.7 226 2 US-09-462-245-2 Sequence 59.7 431.6 Sequence 59.7 59.6 Sequence 59.7 59.7 59.7 59.7 59.7 59.7 59.7 59.7	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	
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ALIGNMENTS

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COUNTRY: USA
ZIP: 10174
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAILIBLE
PARTING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REFERENCE/DOCKET NUMBER: 4324.204-US
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                        US-08-886-765-2
                                                                                    Query Match
Best Local S
                                                                     Matches
                                                                                                                                                                                               TELEFAX: 212-878-9033
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58175000 No. 5817500disk of No. 5817500th America,
STREET: 405 Lexington Avenue
                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                           TYPE: amino acid
                  1 MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                      Similarity
                                                                   100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                         protein
                                                                   <u>,</u>
                                                                   Score 1238; DB 1;
Pred. No. 7.9e-110;
; Mismatches 0;
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                                                                                                   Length
                                                                                                       225;
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US-09-115-660-2
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US-09-115-660-2
                                                                                                                                                                                                                Query Match
Best Local S
Matches 225
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Patent No. 6245546
                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hansen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knap, II
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-0-155
TELEPHONE: 212-878-9655
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                    121 VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
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                                                                       61 LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                                                                                                   1 MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
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                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                           LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
                                                                                                                                            MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
 VENFGTYDPSSGATDLGTVECDGS1YRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
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Mullertz, Anette
Knap, Inge Helmer
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                                                                                                                                                                                                                100.0%; Score 1238; DB 2; llarity 100.0%; Pred. No. 7.9e-110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                     212-867-0123
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                                                                                                                                                                                                                                                   Length 225;
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US-09-570-856B-23
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09570856B Patent No. 6682923
                                                                    NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 194
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6682923
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RET/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
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ORGANISM: Thermomyces lanuginosus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE LOCATION: (1)..(1)
OTHER INFORMATION: "Xaa" at position 1 is
                                      ORGANISM: Paecilomyces variotii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGYARITVADVG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEGVYOPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152
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Pred. No. 3.6e-95;
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61

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4

Query Match

DB 2;

Length 194;

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GENERAL INFORMATION:

APPLICANT: Bentzien, Joerg M

APPLICANT: Dahiyat, Bassil I

TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE FILE REFERENCE: A-67478-1/RFT/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/570,856B

CURRENT APPLICATION NUMBER: US 60/133,714

PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 199-05-12

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.1

SEQ ID NO 29

LENGTH: 221

TYRE: PRT

ORGANISM: Cochliobolus carbonum

US-09-570-856B-29
                                                                                                                                                         RESULT 6
US-08-458-023B-4
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US-09-570-856B-29
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                                                                                                                    Sequence 4, Application US/08458023B Patent No. 5667990
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09570856B Patent No. 6682923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Yoder, Wendy

APPLICANT: Takagi, Shinobu

APPLICANT: Boominathan, Karuppan C.

TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                               121 VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169;
                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                        61 LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
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                                                                                                                                                                                                                                                                                                                                                                                   GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNSYLAVYGWTRNPLVEYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVSPTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVGFTFVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 92
                                                                                                                                                                                                                                                                                                           VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGYARITVADVG
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                                                                                                                                                                                                                                 VNMKTHFDAWASKGMNL-GOHYYQIVATEGYFSTGNAQITV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.1%; Score 806.5; DB 2; 67.9%; Pred. No. 8.4e-69; tive 26; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225
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Pred. No. 6e-84;
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GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: SUMIDA, NAOMI
APPLICANT: SUMIDA, NAOMI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 223
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Best Local Similarity
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APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31.274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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INFORMATION FOR SEQ ID NO:
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LENGTH: 227 amino acids
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGNGYLAVYGWTRNPL 119
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XGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVGGSVNMQNHFNAWQQHGMPL-GQHYYQVVATEGYQSSGBSDIYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.6%; Score 688.5; DB 1; 55.8%; Pred. No. 1.5e-57;
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FOR MASS-PRODUCING
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Sequence 2, App-
No. 583751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/121,436A
FILING DATE: 16-SEP-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-UN-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                     FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
                                                                                                                                          APPLICATION NUMBER: US 07
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
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CITY: W
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Local Similarity 56.7%;
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY
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1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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Nevalainen, Helena
Saarelainen, Ritva
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                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                 US 07/889,893
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                                                                                                                              US 07/524,308
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; MOLECULE TYPE: protein US-08-121-436A-2
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Best Local Similarity
Matches 128; Conserv
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             APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1550.0540003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
PILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTE: STREET: 1100 NEW YORK AVENUE, SUITE CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 TNLEGGTYBISWGDGGNLVGGKGWNPGLNARAIHPEGVYQPNGNSYLAVYGWTRNPLVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEY
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FAGERSTR M, RICHARD
SUOMINEN, PIRKKO
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LANTTO, RAIJA
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M NTYL , ARJ
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(202)
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DRK AVENUE, SUITE 600
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                                                                                                                                                                                                                                                                                                   Version
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; LOCATION: 1..261
; OTHER INFORMATION:
US-08-768-373-2
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US-09-849-242A-2
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GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 128;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US 08/768,373
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 261 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                             SUOMINEN, PIRKKO
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVVQPNGNSYLAVVGWTRNPLVEYY 119
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                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                       STATE: DC
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1..261
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MONTYLO, ARJA
VEHMAANDERO, JARI
LANTYO, RAIJA
LAHTINEN, TARJA
PAGERSTRYM, RICHARD
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                                                                                                                                            Version
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GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Makoto Yaguchi
APPLICANT: David R. Rose
ITITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
ITITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: /label= XINA ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-849-242A-2
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US-08-044-621D-29
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Best Local Similarity
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                                      ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                    STREET: Suit
                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 VVESFGTYDPSTGATRMGSVTTDGGTYNIYRTQRVNAPSIEGTKTFYQYWSVRTSKRTGG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 LESGGQYSVTWSGNGNWVGGKGWNPGTDNRVINYTADYRPNGNSYLAVYGWTRNPLIEYY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVGFTPVALAALAATGALAFPAGNATELEKROT-TPNSEGWHDGYYYSWWSDGGAQATYT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVNFSTLFLAASTAALAAAAPS-----IEKROTLTSSATGTHNGYYYSFWTDGOGNIRFN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVTMANHFNAWRQAGLQL-GSHDYQIVATEGYYSSGSATVNV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: CBS730.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Chaetomium thermophilum
                                                                                                           Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.8%;
    PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
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Pred. No. 1.6e-56;
No. matches 56;
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WordPerfect 5.1

US/08/044,621D

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US-08-709-912-9

; Sequence 9, Application US/08709912

; Patent No. 5759840
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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-29
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/04
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE .... Proce
DESCRIPTION: Proce
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKCANISM: Schizophyllum commune STRAIN: Schizophyllum commune, >
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDEDNESS: No.
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 613-563-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL: Canadian Fed. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                    183
                                                                                                                                  208
                                                                                                                                                                     123
                                                                                                                                                                                                  153 RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
                                                                                                                                                                                                                                                                                                                                                                      119; Conservative
                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                      34 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 92
                                                                                                                                                                                                                                                                                                       3 TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1988
                                                                                                                                                                                                                                     YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW
                                                                                                                                    TEGYFSSGYARITY 221
                                                                                                                                                                   RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
                                                                                                    TEGYOSSGTATITV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abstract 676
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                                                                                                                                                                                                                                                                                                                                                                      53.6%; Score 663; DB 1; Length 197; 61.3%; Pred. No. 3.2e-55; tive 26; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5405769 Relevant
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183

TEGYOSSGTATITV 196

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JOURNAL: Jurasek, L

JOURNAL: Canadian Fed. Biol. Soc. annual meeting

PAGES: Abstract #676

JATE: 1988

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Yaguchi Dr., Kazuhiko
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Oku, T
AUTHORS: Yaguchi, M
AUTHORS: Parse, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Schizophyll STRAIN: Xylanase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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          208
                                                              153 RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
                                          123 RYNAPSIDGTOTFEOFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA 182
                                                                                                                                                                               63
                                                                                                                                10172-0194
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TEGYFSSGYARITV 221
                                                                                                              YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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277 Park Ave.
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                                                                                                                                                                                                                                                  26;
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Pred. No. 3.2e-55;
Rismatches 43
                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                   Length 197;
                                                                                                                                                                                                                                                    Indels
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US-09-047-370-9
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                                                                                                                       Matches
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           TOPULACION TYPE: process.
MOLECULE TYPE: process.
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 758-29 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
PILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
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APPLICANT: Sung D
                                                                                                                                                                                       STRAIN: Xylanabo...
STRAIN: Xylanabo...
PUBLICATION INFORMATION:
AUTHORS: Oku, T
AUTHORS: Yaguchi, M
AUTHORS: Parse, M
AUTHORS: Durasek, L
TOURNAL: Canadian Fed. Biol. Soc. annual meeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Modification of Xylanase to Improve TITLE OF INVENTION: Thermophilicity, Alkalophilicity and TITLE OF INVENTION: Thermostability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLECUPAL: 1212
                                                                                                                                                                                                                                                                                                                   ORGANISM: SCHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
10172-0194
                                                                      TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 92
                                                   TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS 62
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277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Ploppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Schizophyllum commune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758-2400
                                                                                                                                     53.6%;
61.3%;
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                                                                                                                   26;
                                                                                                                  Score 663; DB 1; Length 197; Pred. No. 3.2e-55; Mismatches 43; Indels
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US-09-570-856B-18
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                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08768373 Patent No. 6228629
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: PALOHEII
APPLICANT: HAKOLA,
APPLICANT: M NTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: POSEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Applica Patent No. 6682923 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Schizophyllum commune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 197
                                                                                                                                                                         APPLICANT:
                                                                                           APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES,
TITLE OF INVENTION: AND USES THEREOF
                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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  STREET:
                                      ADDRESSEE:
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SEE: STERNE, KESSLER, GOLDSTEIN & 1100 NEW YORK AVENUE, SUITE 600 WASHINGTON
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M NTYL , ARJ
                                                                                                                                                                                            VEHMAANPER , JARI
LANTTO, RAIJA
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                                      FOX, P.L.L.C.
                                                                                                                     ENCODING THEM
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COUNTRY: US
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US 60/08,746
PLING DATE: 17-DEC-1996
CLASSIFICATION NUMBER: US 60/008,746
PRIOR APPLICATION NUMBER: US 60/020,839
PILING DATE: 18-DEC-1995
PRIOR APPLICATION NUMBER: US 60/020,839
PILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET 
Search completed: February 10, 2006, 15:03:36 Job time : 39.1265 BecB
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NAME/KEY: Protein
LOCATION: 1..230
OTHER INFORMATION: /label= XLNB
US-08-768-373-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.5%; Score 662.5; DB 2; Length Best Local Similarity 58.8%; Pred. No. 4.4e-55; Matches 130; Conservative 23; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chaetomium thermophilum STRAIN: CBS730.95
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1238
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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              US-09-467-368-2
US-10-237-386-24
US-11-088-725A-46
US-11-088-725A-46
US-10-237-386-20
US-10-425-115-267585
US-10-425-115-267585
US-10-425-115-261946
US-10-237-386-25
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633 51.1 189 4 US-10-307-441-19 632.5 51.1 199 4 US-10-307-441-17 632.5 51.1 199 4 US-10-307-441-17 632.5 51.1 190 6 US-11-088-725A-42 632.5 51.1 190 6 US-11-088-725A-42 632.5 51.1 223 4 US-10-237-386-34 631.5 51.0 223 4 US-10-237-386-33 634.5 50.9 190 4 US-10-237-386-33 624.5 50.9 190 6 US-11-088-725A-1 613.5 49.6 31.3 US-10-213-990-72 611.5 49.4 217 3 US-10-29-393-2 610.5 49.3 223 4 US-10-29-393-2 610.5 49.3 223 4 US-10-29-393-2 599.5 48.4 221 4 US-10-237-386-37 573 46.3 228 4 US-10-237-386-37 586 45.9 189 6 US-11-088-725A-40	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	į
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	40,	<u>1</u> 3,	42,	39,	37,	2	2	11,	72,	1		36,	34,	42,	17,	28,	19,	
19, App. 17, App. 34, App. 34, App. 34, App. 37, App. 17, App. 18, App. 19, App. 19, App. 11, App. 19, App. 11,	App	App	Āpp	App	App	Appl	Iddy	App	App	App1	Αpp	App	App.	App	App	App	App	

US-09-467-368-2

Sequence 2, Application Patent No. US200201600 GENERAL INFORMATION:

Application US/09467368

ALIGNMENTS

APPLICANT: Hansen,

Wagner, Peter Mullertz, Anette Peter

US-09-467-368-2 Query Match Best Local Similarity Matches 225; Conserv INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 225 amino acids TYPE: amino acid STREET: 405 Lexington Avenue CITY: New York STATE: NY COUNTRY: USA ZIP: 10174 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: FastSEQ for Windows Version 2.4 CURRENT APPLICATION NUMBER: US/09/467,368 FILING DATE: 21-Dec-1999 CLASSIFICATION: CUnknown> PRIOR APPLICATION DATA: APPLICATION UNMBER: US/08/886,765 APPLICATION UNMBER: US/08/886,765 APPLICATION UNMBER: US/08/886,765 APPLICATION UNMER: 33,728 REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 4324.204-US TELEPHONE: 212-867-0123 TELEPHONE: 212-867-0123 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: Knap, Inge Helmer TITLE OF INVENTION: Animal Feed Additives NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600 TELEFAX: 212-878-9655 100.0%; Score 1238; DB 3; ilarity 100.0%; Pred. No. 1.6e-109; Conservative 0; Mismatches ^-2.0 Length 225;

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; SEQ ID NO 24
; LENGTH: 225
; TYPE: PRT
; ORGANISM: T.
US-10-237-386-24
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CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0005585.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR TILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin version 3.0
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                                                                                Sequence 20, Application US/10307441 Publication No. US20030166236A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: SUNG, Wing L.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen,
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Sorensen, Jens
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100.0%; Pred. No. 1.6e-109;
ative 0; Mismatches 0;
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APPLICANT: Logen Bio-Products Corporation

APPLICANT: White, Theresa C

APPLICANT: Giroux, Genevieve R

APPLICANT: Wallace, Katie B.A.

TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression

FILE REFERENCE: Q80712

CURRENT APPLICATION NUMBER: US/11/088,725A

CURRENT FILING DATE: 2005-03-25

PRIOR APPLICATION NUMBER: US 60/556,061

PRIOR APPLICATION UMBER: US 60/556,061

PRIOR FILING DATE: 2004-03-25

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIn version 3.2
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CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 194
TYPE: PRT
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US-11-088-725A-46
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Best Local Similarity
                                                                                                                                                                                                                         Matches 194;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                      LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                              Local Similarity
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                                                                                        92 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 151
                                                                                                                                                                                  32 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91
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    TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
                                                                 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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100.0%; Pr.
                                                                                                                                                                                                                           87.9%; Score 1088; DB 6;
100.0%; Pred. No. 2.5e-95;
tive 0; Mismatches 0;
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Sequence 20, Application US/10237386

Publication No. US20030180899A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbeen, Ole
APPLICANT: Sibbeen, Ole
APPLICANT: Sibbeen, Ole
CURRENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66
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APPLICANT: Sibbeen, Jens
TITLE OF INVENTION: Xylange Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Best Local Similarity
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APPLICANT: Sibbesen,
APPLICANT: Sorensen,
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Pred. No. 7.3e-70;
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; LENGTH: 221
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US-10-425-115-221836
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5:5222)B
CURRENT APPLICATION UNMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 221836
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 221836, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: MRT4577_133906C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                       116
 180
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                                                                                                                                        61 VTYTNGAGGSYSVNWGSGGNFVGGKGWNPG-SARTVTYSGSYNPNGNSYLAIYGWTRNPL
                                                                                                                                                                       56 ATYTNIEGGTYEISWGDGGNIVGGKGWNPGINARAIHFEGVYQPNGNSYLAVYGWTRNPL 115
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 RSSGSVNMKTHFDAWASKGMTL-GSHYYQIVATEGYFSTGSASITV
                      RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
                                                                                                   VEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
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                                                                    VEYYVVENFGTYDPSSQASNKGTVTADGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNK
                                                                                                                                                                                                            MVSFTSLITAAVAATGAFAAPATDVAARSSGDLVARQSTPNAEGTHNGCFYSWWTDGGSK
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63.7%;
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                                                                                                                                                                                                                                                                                                   Score 794.5; DB (
Pred. No. 2.7e-67)
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Pred. No. 1.9e-68;
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RESULT 9
US-10-237-386-22
(S-10-237-386-22
; Sequence 22, Application US/102:
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; ORGANISM: A. US-10-237-386-22
                                                                                                                             APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Ser
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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US-10-425-115-267585
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yingwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 267585
LENGTH: 221
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Best Local
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                                                                                        SOFTWARE: P
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                                            LENGTH: 22
TYPE: PRT
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LOCATION: (1)..(221)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                             PatentIn version 3.0
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; Pred. No. 7.9e-67;
26; Mismatches 45;
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APPLICANT: Danisco A/S APPLICANT: Sibbesen, Ole APPLICANT: Sorensen, Jens

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RESULT 11
US-10-237-386-26
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 361946
LENGTH: 234
                  Sequence 26, Application US/10237386 Publication No. US20030180895A1
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Plants
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                              GGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVSFTSIFTAAVAATGALAVPVTDLATRSLGALTARAGTPSSQGTHNGCFYSWWTDGGAQ
                                                                                                                                                                        RODKRISGIVQIGCHFDAWARAGLNVNGDHYYQIVAIEGYFSSGYARITV 221
                                                                                                                                                                                                                                                                                          GGAQATYTNEAGGKYSVNWKTGGNMVGGKGWNPGA-ARTITYSGTYSPQGNSYLAIYGWT 119
                                                                                                                                                                                                                                                                                                                                                                       MVSFTTVITAAVAATGALAAPVADASTDFAERSLSVLTARAGTPSSQGTHNGCFYSWWTD 60
                                                                                                                                                                                                                                                                                                                                                                                                         MVGFTPVALAALAATGALAFPAGNATE-----LEKROTTPNSEGWHDGYYYSWWSD
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                                                                                                                                                                                                              RNPLVEYYVVENFGTYDPSSAASVKGSVTADGSSYKIAQTQRVNQPSIDGTKTFNQYWSV
                                                                                                                                  RONKRSSGSVNMKTHFDAWASKGMOL-GOHNYQIVATEGYFSSGSSSITV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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65.5%; Pred. No. 1.7e-65;
tive 25; Mismatches 46
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Pred. No. 3.5e-65;
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; LENGTH: 231
; TYPE: PRT
; ORGANISM: C.
US-10-237-386-26
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APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Jens
APPLICANT: Sibbesen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Sequence 25, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                       SEQ ID NO 25
LENGTH: 231
TYPE: PRT
ORGANISM: C.
JS-10-237-386-25
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CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: FCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
                                                                                                                                                    Best
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                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 57.9%; Score 716.5; DB 4; Local Similarity 58.7%; Pred. No. 7.4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                  Similarity
                                                        MVGFTPVALAALAATGALAFPAG------NATE-LEKRQTTPNSEGWHDGYYYSWWSD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQQKRVGGSVNMQNHFNAWSRYGLNL-GQHYYQIVATEGYQSSGSSDIYV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RODKRISGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPLVEYYVIESYGTYNPSSGAQVKGSFQTDGGTYNVAVSTRYNQPSIDGTRTFQQYWSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSV 171
                             MVSFKSLLLAAVATTSVLAAPFDFLRERDDVNATALLEKROSTPSAEGYHNGYFYSWWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGSAQYTMGEGSRYSVTWRNTGNFVGGKGWNPG-TGRVINYGGAFNPQGNGYLAVYGWT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVSFKSLLLAAVATTSVLAAPFDFLRERDDGNATALLEKROSTPSSEGYHNGYFYSWWTD 60
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                                                                                                                                               56.7%; Score 701.5; DB 57.4%; Pred. No. 2e-58;
                                                                                                                           31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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                                                                                                                                                                        DB 4;
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                                                                                                                                                                      Length 231;
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; TYPE: PRT
; ORGANISM: C:
US-10-237-386-29
                                                                                                                                                                                       US-10-237-386-27
US-10-237-386-27
US-10-237-386
Publication No. US20030180895A1
Publication No. US20030180895A1
Publication No. US20030180895A1
Publication No. US20030180895A1
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US-10-237-386-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sornesen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor:
FILE REPERENCE: 674509-2046
CURRENT ERPERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
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APPLICANT: Solbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Solbesen, Ole
APPLICANT: Sovensen, Ole
APPLICANT: Sovensen, Ole
APPLICANT: Sovensen, Ole
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: CT/IB01/00426
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER: OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YYIVENEGTYDESSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTEDQYWSVRQDKRT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133;
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                                                                                                                                                                                                                                                                                                                                                                                                     SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYIVESFGTYDESSQASKFGTIQQDGSTYTIAKTTRVNQPSIEGTSTFDQFWSVRQNHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVSFKAL---LLGAAGALAFPF-NVTQMNELVARAGTPSGTGTNNGYFYSFWTDGGGTVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGSAQYIMGEGSRYSVIWRNIGNFVGGKGWNPG-SGRVINYGGAFNPQGNGYLAVYGWT 119
                                                                                                                                                                                                                                                                                                                                                               SGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQSSGSSSITVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%; Score 691.5; DB 4 llarity 59.1%; Pred. No. 1.7e-57; Conservative 29; Mismatches 54
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9

Gaps

219

175

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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTMARE: Patentin version 3.0
SEQ ID NO 27
LENGTH: 227
TYPE: PATE ORGANISM: H. insolens
US-10-237-386-27
                                                                                                                                                                                                                                                                                                                    ; LENGTH: 241
; TYPE: PRT
; ORGANISM: C:
US-10-237-386-35
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US-10-237-386-35
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APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Jens
APPLICANT: Sorensen, Jens
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
TITLE OF INVENTION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 000585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/10237386 Publication No. US20030180895A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.7%; Score 689.5; DB 4; Length Best Local Similarity 55.8%; Pred. No. 2.7e-57; Matches 126; Conservative 31; Mismatches 62; Indels
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                          / Match 55.7%; Score 689; DB 4; Length 241; Local Similarity 59.5%; Pred. No. 3.3e-57; Local 31; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 RVGGSVNMQNHFNAWQQHGMPL-GQHYYQVVATEGYQSSGESDIYV 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VEYYVIESYGTYNPGSQAQYKGTFYTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKNK 179
120 IVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
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                                          NEAGGQYSVTWSGNGNWVGGKGWNPG-SARTINYTANYNPNGNSYLAVYGWTRNPLIEYY 118
                                                                                       NLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
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Db 119 VVENFGTYNPSTGATRLGSVTTDGSCYDIYRTQRVNQPSIEGTSTFYQFWSVRQNKRSGG 178

Qy 180 TVQTGCHPDAWARAGLNVNGDHYYQIVATEGYPSSGYARITV 221
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179 SVNMAAHFNAWAAAGLQL-GTHDYQIVATEGYYSSGSATVNV 219

Search completed: February 10, 2006, 15:22:35 Job time: 132.563 secs

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Result
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					Appl Appl Appl Appl	Appl Appl Appl Appl

; SOFTWARE: Pate ; SEQ ID NO 24 ; LENGTH: 225 ; TYPE: PRT ; ORGANISM: T. US-11-170-653-24 Sequence 24, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION: APPLICANT: Danisco A/S APPLICANT: Sibbesen, Ole APPLICANT: Sibbesen, Ole APPLICANT: Sovensen, Jens TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor: FILE REFERENCE: 674509-2046 FULDENTE INVENTION NUMBER: US/11/170,653 CURRENT APPLICATION NUMBER: US/11/170,653 CURRENT APPLICATION NUMBER: US/10/237,386 PRIOR APPLICATION NUMBER: DCT/IB01/00426 PRIOR APPLICATION NUMBER: CB 0005585.5 PRIOR APPLICATION NUMBER: GB 001575.1 Query Match Best Local Similarity Matches PRIOR APPLICATION NUMBER: GB 0015751.1 PRIOR FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 66 181 121 121 13 225; 61 LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI μ 1 MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN PatentIn version 3.0 VQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG VENPGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT lanuginosus Conservative 100.0%; Score 1238; DB 7; 100.0%; Pred. No. 4.7e-106; tive 0; Mismatches 0; Length 225; Indels 225 0, Gaps 180 180 120 120 60

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APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
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FILE REFERRNCS: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GT/1801/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
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SOFTWARE: Patentin version 3.0
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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Applica Publication No. US20 GENERAL INFORMATION:
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SEQ ID
                                                                                                                                                                                                                        APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2005-06-23
                                                                                                                                                                                                                                                                                                                               APPLICANT: Danisco A/S APPLICANT: Sibbesen, (APPLICANT: Sorensen, (APPLICANT: Sorensen, (APPLICANT: Sorensen, (APPLICANT)
                  NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn versi
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US-11-170-653-22
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Best Local Similarity
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APPLICANT: Sibbesen,
APPLICANT: Sorensen,
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Al:
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION UNMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION UNMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.1
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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TYPE: PRT
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176 RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                         116 VEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
                                                                    120 IBYYVVENEGTYDESSQATVKGSVTADGSSYKIAQTQRTNQESIDGTQTEQQYWSVRQNK
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                                                                                                                                                                        61 ATYTNGAGGSYSVNWKTGGNLVGGKGWNPGA-ARTITYSGTYSPSGNSYLAVYGWTRNPL
                                                                                                                                                                                               56 ATYTNILEGGTYEISWGDGGNLVGGKGWNPGLNARAIHPEGVYQDNGNSYLAVYGWTRNPL 115
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                                                                                                                                                                                                                                                                                                                                                                          Score 775.5; DB 7
Pred. No. 7.4e-64;
25; Mismatches 46
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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; LENGTH: 231
; TYPE: PRT
; ORGANISM: C.
JS-11-170-653-26
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Publication No. US20050271769A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
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Sorensen, Jens
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58.7%; Pred. No. 1.8e-58;
tive 29; Mismatches 55
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; LENGTH: 231
; TYPE: PRT
; ORGANISM: C.
US-11-170-653-25
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; Sequence 29, Application US/11170653
; Publication No. US20050271789A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: C. US-11-170-653-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity 57.4%;
Matches 132; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
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APPLICANT: Sorensen, Jens
APPLICANT: Sorensen, Jens
TITLE ON THE SORENSEN APPLICANT: SORENSE Variants Having Altered Sensitivity to Xylanase Inhibitor.
FILE REFERENCE: 674599-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 0015751.1
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APPLICANT: Sibbesen,
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                             178
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                                                                          116 YYIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTRVNQPSIEGTSTFDQFWSVRQNHRS
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                                                                                                                                                                      57 YQNGAGGSYSVQWQNCGNFVGGKGWNPGA-ARTINFSGTFSPQGNGYLAIYGWTQNPLVE 115
                                                                                                                                                                                                                     58
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SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA 222
                                                                                                     YYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRT 177
                                                                                                                                                                                                                YTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVE 117
                                                                                                                                                                                                                                                                  MVSFKAL---LLGAAGALAFPF-NVTQMNELVARAGTPSGTGTNNGYFYSFWTDGGGTVN 56
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Pred. No. 4.2e-57;
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; TYPE: PRT
; ORGANISM: H.
US-11-170-653-27
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US-11-170-653-35
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         PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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Publication No. US20050271769A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Sequence 35, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
                                                                                                                                                                                                TITLE OF INVENTION: Xylanse Variants Having Altered FILE REFERENCE: 674509-2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGNGYLAVYGWTRNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 ATYTNIEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL 115
SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     VEYYVIESYGTYNPGSQAQYKGTFYTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKNK 179
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Sorensen, Jens
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Pred. No. 5.2e-56;
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; TYPE: PRT
; ORGANISM: C:
US-11-170-653-35
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; TYPE: PRT
; ORGANISM: T.
US-11-170-653-31
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LENGTH: 241
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NUMBER OF SEQ ID NOS: 66
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT EPPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2005-06-23
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PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
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                                                                                                   119 YIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS
                                                                                                                                                                                                      59 TNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY 118
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GTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEAGGOYSVTWSGNGNWVGGKGWNPG-SARTINYTANYNPNGNSYLAVYGWTRNPLIEYY 118
                                                             YIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSS
                                                                                                                                                                      TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEY 120
                                                                                                                                                                                                                                                                               55.7%; Score 689; DB 7;
59.5%; Pred. No. 6.1e-56;
tive 31; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                              55.3%; Score 684.5; Db /; 57.1%; Pred. No. 1.4e-55; 7.1%; Orent Mismatches 61;
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RESULT 12
US-11-170-653-32
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US-11-170-653-30
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; ORGANISM: T.
US-11-170-653-30
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CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR PILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION:
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SOPTWARE: PatentIn version 3.0
SEQ ID NO 30
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT PILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REPERENCE: 674509-2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSVNTANHFNAWAQQGLTL-GTMDYQIVAVEGYFSSGSASITVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THIEGGTYBISWGDGGHLYGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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; TYPE: PRT
; ORGANISM: S.
US-11-170-653-23
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; TYPE: PRT
; ORGANISM: T.
US-11-170-653-32
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US-11-170-653-23
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APPLICANT: Sibbeen, Jens
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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SOFTWARE: PatentIn versic
SEQ ID NO 32
LENGTH: 222
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 66
                                                                        153 RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
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                                                                                                                                                                                                                                           34 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH
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                                                                                                                                             FEGYYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152
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                                                                                                                     YSGTYOPNGNSYLSVYGWTRSSLIBYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW
                                                                                                                                                                                                                TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS
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                            RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
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                                                                                                                                                                                                                                                                                                    53.6%; Score 663; DB 7; Length 201; 61.3%; Pred. No. 1.2e-53; tive 26; Mismatches 43; Indels
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TEGYFSSGYARITY 221

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US-11-10-653-28
US-11-170-653-28

Sequence 28, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:
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US-11-170-653-44
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Matches 12
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SEQ ID NO 44
LENGTH: 221
TYPE: PRT
ORGANISM: A. OTYZBE
3-11-170-653-44
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Best Local S
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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
APPLICANT: Danisco A/S
APPLICANT: Soibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Soibbesen, Ole
APPLICANT: Sovensen, Jens
TITLB OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
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CURRENT FILING DATE: 2005-06-23
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
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PRIOR FILING DATE: 2002-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 53.4%; Score 660.5; DB 7; al Similarity 56.1%; Pred. No. 2.2e-53; 125; Conservative 34; Mismatches 59;
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Search completed: February Job time : 12.2768 secs 10, 2006, 15:23:01

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.

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ALIGNMENTS

Thermomyces lanuginosus xylanase, Xyn 16-MAY-2002 AAE18456; AAE18456 standard; protein; 194 (first entry) ₽

Modified xylanase; thermostability; alkalophilicity; pulp manufacture; poultry; swine feed; enzyme; Xyn. industrial process;

Thermomyces lanuginosus.

WO200192487-A2.

06-DEC-2001.

31-MAY-2001; 2001WO-CA000769.

31-MAY-2000; 2000US-0213803P.

(CANA) NAT RES COUNCIL CANADA

Sung

WPI; 2002-171435/22.

manufacturing. Modified xylanase exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp

Disclosure; Page 83-84; 109pp; English.

The present invention relates to a modified xylanase exhibiting increased thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to corresponding native xylanase. The present sequence is Thermomyces corresponding native xylanase. lanuginosus xylanase, Xyn

Sequence 194 AA;

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                                                                                                                                                                                   monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermonges xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed
                                                                                                                                                                                                                                                                                         This sequence represents the Xylanase from Thermomyces lanuginosus strain DSM 4109. This Xylanase, and Xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssochlamus or Paecilomyces strains can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungal xylanase prepns. for use as animal feed additives - construct for producing recombinant Thermomyces xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 45-46; 69pp; English.
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                                                                                                                                                          The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pyES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amplase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS
                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bread improving additive alpha-amylase, increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-477123/47
N-PSDB; AAT43010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endo-1,4-beta-D-xylanase; xylanase;
Humicola lanuginosa; bread; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endo-1,4-beta-D-xylanase
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22-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 31-32; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jorgensen OB,
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                                                                                                                                      field)
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(first entry)
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     DB 2;
.2e-98;
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                                                                   The present sequence is the protein sequence of a thermostable xylanase of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm) of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, phytase, protease, galactanase, mannanase, deaxtranase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soys, wheat, barley, oats and/or rye
                                                                                                                                                                                                   Composition useful as an animal feed additive comprises at least two thermostable enzymes selected from endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase
                                                Sequence
                                                                                                                                                                                Disclosure; Page 60-61;
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                                                                                                                                                                                                                                                                                                     ROCHE VITAMINS
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nilarity 100.0%;
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Best Local Similarity
Matches 194; Conserv

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Score 1088; DB 9; Pred. No. 2.2e-98;

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                                                                                                                                                              which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is useful in the mashing and filtration steep in brewing the composition is the mashing and filtration steep in brewing the composition is the mashing and filtration steep in brewing the composition is the mashing and filtration steep in brewing the composition is the mashing and filtration steep in brewing the composition is the mashing and the composition is the composition of the composition is the composition of the composition o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a process for preparing a mash (A) (having enhanced filterability and/or improved extract yield after filtration)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of a mash (having enhanced filterability and/or improved extract yield after filtration) comprises preparing a mash in the presence of enzyme activities comprising xylanase of GH family 10 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-458778/46.
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                                                                                        process of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Festersen RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2003; 2003DK-00001895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylanase SEQ ID NO:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   filtering to obtain wort.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB00305 standard; protein;
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                                                                                                                                  The present sequence represents a xylanase used in the mashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viksoe-Nielsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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Best Local S
Matches 193
                                                                                                                                                                                 The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                   Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB48543 standard; protein; 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermomyces lanuginosus xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB48543;
                                                                                                                                                           Sequence 194
                                                                                                                                                                                                                                                                                           Disclosure; Fig 16L; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-679800/66.
                                                                                                                                                                                                                                                                                                                                                                                                  Bentzien JM;
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                                                                                                     tch 99.5%; So
al Similarity 100.0%; I
193; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRVNAPSIDGTQTFDQYMSVRQDKRTSGTVQTGCHFDAMARAGLAVNGDHYYQIVATEGY
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                                                  TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
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                FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
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                                                                                                    Score 1083; DB 3; ; Pred. No. 5.5e-98; 0; Mismatches 0;
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                                                                  Matches
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                                                                                                                                                              activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, and has been modified to exhibit relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
starch extraction; food thickener; animal food additive; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 9
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 16L; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in food and anim alkalophilicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2001; 2001WO-US048018
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                                                                                                                                  Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-2000; 2000US-00710050
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                                                                                 Local Similarity
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TTPNSEGMHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
                                 TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
                                                                  Conservative
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                                                                                                 Length 194;
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                                                                                                                Query Match
Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                  The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a blaaching agent comprising the XA protein. The nonnaturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, or 144. The non-naturally occurring xylanase activity (XA) protein is also useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species inclinated inclinate from another species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                       Sequence 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 24; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-118575/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bentzien J, Dahiyat
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07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper industry; food; animal feed; thermostability; alkalinophilic;

    lanuginosus xylanase.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI66751 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hot alkali treatment.
                                                                                                                Local Sir
hes 193,
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                                        TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF
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99US-0138156P.
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100.0%; Pr
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0: Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 16K; 114pp; English.
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                                                                                                                                                                                                       TTPNSEGWHDGYYYSWWSDGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH
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                                                                                                                             FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                                                                                                                                                                             TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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|SSGYARITVADVG
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                                                                                         FTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQST
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                                                                                                                                                                                                                                                                                                                  Score 965; DB 3;
Pred. No. 2.2e-86;
1; Mismatches 13
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                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 169
                                                                                                                                                                                                                                                                                                                                                                                                                                   alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P variotii xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 16K; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alkalophilicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel xylanase activity protein, useful in bleaching process of pulp in food and animal feed industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2001; 2001WO-US048018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paecilomyces variotii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   starch extraction; food thickener; animal food additive; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                              Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-608200/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bentzien J, Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (XENC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-2000; 2000US-00710050.
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                                                                                                                                                                                                                                                                                   Similarity
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                                FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121
   FTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQST
                                                                                                                            TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH
                                                                                                                                                         TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAIH 61
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                   88.7%;
87.6%;
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                                                                                                                                                                                                                                              Score 965; DB 5;
Pred. No. 2.2e-86;
L1; Mismatches 13
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TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH

FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIH

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Best Loc Matches

169;

Conservative

Query Match Best Local Similarity

88.7%; Score 965; DB 8; 87.6%; Pred. No. 2.2e-86; 11; Mismatches

Length 194; Indels

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                                              The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The nonnaturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, 67, 194. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species
 Sequence 194 AA;
                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                             New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-118575/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paecilomyces variotii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper_industry; food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. variotii xylanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI66750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI66750 standard; protein; 194
                                                                                                                                                                                                                                                                                                                                             bleaching (paper) pulp, and in the food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XENC-) XENCOR
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                                     included
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSGYARITVADVG 194
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                                     for comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahiyat BI;
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99US-0138156P.
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 16Q; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB48548 standard; protein; 221 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bleaching agent.
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                                                                                                                                                                                                                                                                                     QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAI
TRTNOPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMNL-GQHYYQIVATEGY
                                      TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                                        QNTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGYARITVADVG 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGYARITVADVG 194
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                                                                                                                                                                                                                                                                                                                                                                                              68.2%;
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; Pred. No. 2.2e-64;
22; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 16Q; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-608200/65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C carbonum xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200238746-A2
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TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
                                                                                                    TYSGTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYDPSSQSQNKGTVTSDGSSYKIAQS
                                                                                                                                               HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                                  QNTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
                                                                                                                                                                                                                                                                                                  QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        68.2%; Score 742; DB 5; 70.0%; Pred. No. 2.2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                              Mismatches
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RESULT 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66732. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, 67, 194. The non-naturally occurring xylanase activity (XA) protein is also useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 29; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 221 AA;
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                                    HPEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSTGNAQITV 218
                                                                                                                             ONTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
      TYSCTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYDPSSQSQNKGTVTSDGSSYKIAQS
                                                                                                                                                              QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
                                                                                                                                                                                                                                                          Conservative
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99US-0138156P.
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food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                       68.2%; Score 742; DE 70.0%; Pred. No. 2.26 tive 22; Mismatches
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                                                                                                                                                                                                                                                                                        DB 8;
2.2e-64;
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FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121

TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH

62 61

YSGTYOPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW

122

Matches

119;

Conservative

26;

43;

Indels

6

Gaps

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ID ARAGEO
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XX ARAGE
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XX Pamil
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XW EP82E
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Best Local (
                                                                                                                                                                                        AAM60728-44 represent family 11 xylanases. The specication describes a method for modifying a Family 11 xylanase to improve its thermophilicity, alkalophilicity and or thermotolerance. This method comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase II or corresponding aligned amino acids of another Family 11 xylanase, replacement of one or more amino acid sequences in the N-terminal region with corresponding aligned sequences from another Family 11 xylanase to form a chimeric xylanase and/or upstream extension of the N terminus by addition of upto 10 amino acids. The modified xylanses are useful for improving the bleachability of wood pulp by treatment at 55-75 degrees celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-improving animal feed additives. They might also be useful in the processing of wheat or maize for starch production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pamily 11 xylanase; improve; thermophilicity; alkalophilicity;
thermotolerance; bleach; wood pulp; processing; wheat; maize;
digestibilitiy-improving animal feed additive; starch production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified xylanase enzymes - useful for improving wood pulp bleaching,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1996;
                                                                                                                                Sequence 197 AA;
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Result
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ALIGNMENTS

N;Alternate names: xylanase A C;Species: Schizophyllum commune C;Date: 27-Jun-1994 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004 C;Accession: A44597; S41411; A05147; S38973

A;Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33 A;Experimental source: strain Delmar ATCC 38548

A; Molecule type: A; Accession: A44597 A; Reference number: submitted to the Protein

A44593

Sequence Database, March 1994

Residues: 1-197 <YAG>

RESULT 1 A44597

endo-1,4-beta-xylanase (EC 3.2.1.8) A -

bracket fungus (Schizophyllum commune)

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A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degration endo-1,4-beta-xylanase homology cxYL- F;12-197/Domain: endo-1,4-beta-xylanase homology cxYL- F;12-197/Domain: endo-1,4-beta-xylanase homology cxYL- F;11-160/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 83-123 <BRA>
A;Cross-references: UNIPARC:UPI0000172966
R;Paice, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie,
Appl. Environ. Microbiol. 36, 802-808, 1978
A;Reference number: A05147; MUID:79102289; PMID:32833
A;Accession: A05147
                                                                                                                                                                                                                                                                                                                                             A; Experimental source: ATCC C; Function:
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R;Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.; FEBS Lett. 334, 296-300, 1993
A;Title: Amino acid sequence and thermostability of xylanase A from Schizophyllum commune A;Reference number: S38973; MUID:94063044; PMID:8243636
A;Accession: S38973
                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000034D33
A;Experimental source: ATCC 38548
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A;Residues: 1-27 <PAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Identification of a glutamate residue at the active site of xylanase A from A;Reference number: S41411; MUID:94155888; PMID:7906649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bray, M.R.; Clarke, A.J.
Bur. J. Biochem. 219, 821-827, 1994
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Query Match
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Matches 119; Conserv
   Conservative
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61.3%; Pr
tive 26;
Score 663; DB 1;
Pred. No. 5e-47;
6; Mismatches 43
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A;Molecule type: protein
A;Residues: 31-45;82-94;152-160 <YOH>
A;Cross-references: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82; UNIPARC:UPI0000175A83
A;Cross-references: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82; UNIPARC:UPI0000175A83
C;Genetics:
A;Introns: 81/2
C;Function:
A;Pathway: xylan degradation
C;Function:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Superfamily: endo-1,4-beta-xylanase; polysaccharide degradation
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
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                                        RESULT
S57477
endo-1,4-beta-xylanase (EC : N;Alternate names: xylanase
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A;Title: Two family G xylanase genes from Chaetomium gracile and
A;Reference number: S71472; MUID:96118924; PMID:8595661
A;Accession: S71472
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A;Cross-references: UNIPROT:Q12579;
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                                                                                                                                                                                                                                              VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS
                                                                                                                                                                                                                                                                                                             EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                                                      SGTFSPQGNGYLAIYGWTQNPLVEYYIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTR
                                                                                                                                                                                                                                                                                                                                                                      TPSGTGTNNGYFYSFWTDGGGTVNYQNGAGGSYSVQWQNCGNFVGGKGWNPGA-ARTINF
                                                                                                                                                                                                                                                                                                                                                                                           TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF
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                                                                                                                                                              SGYARITVA 191
                                                                                                                                                                                                    VNOPSIEGTSTFDQFWSVRQNHRSSGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glu #status predicted
                     (EC 3.2.1
                                                                                                                        219
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8
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Pred. No. 2.1e-46;
28; Mismatches 42
                       μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIPARC: UPI00000421A6; EMBL: D49850; NID: g1339857;
                     precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                       Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsukagoshi,
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C;Species: Emericella nidulans, Aspergillus n: C;Date: 10-Oct-1995 #sequence_revision 22-Nov C;Accession: S57477 R;Perez-Gonzalez, J.A. submitted to the EMBL Data Library, June 1995 submitted to the EMBL Data Library, June 1995
                                                                                                                                                           A; Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Dalboge, H.; Heldt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A;Title: A novel method for efficient expression cloning
A;Reference number: S43919; MUID:94247364; PMID:8190078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens) C;Species: Humicola insolens C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: S43919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
S43919
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C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
E;1-19/Domain: signal sequence #status predicted <SIG>
F;20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F;48-225/Domain: endo-1,4-beta-xylanase ohmology <XYL>
F;48-225/Domain: endo-1,4-beta-xylanase ohmology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-225 < PER>
A; Cross-references: UNI
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: Expression A;Reference number: S57469 A;Accession: S57477
                                                                                        F;48-225/Domain: endo-1,4-beta-xylanase homology F;112,123,157/Binding site: substrate (Tyr, Tyr, F;121,212/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-227 < DAL>
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                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                           A;Gene: XYL1
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P55334; UNIPARC:UPI00000421A4;
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S43919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                            Query Match
                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116;
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al Similarity
113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSTPSSTGWSNGYYYSFWTDGGGDVTYTNGAGGSYTVQWSNVGNFVGGKGWNPG-STRTI
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                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
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                   59.4%;
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Pred. No. 9.6e-46;
  Pred. No. 1.40
7; Mismatches
                        Score 646; DB 2;
Pred. No. 1.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                       #status predicted homology <XYL>
                                                                                                                    Arg)
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                                                                                                                                                                                                                                                                                                                                                               EMBL: X76047; NID: g505260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal
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Matches

Conservative

2;

Gaps

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A;Accession: $78207
A;Molecule type: protein
A;Cross-references: UNIPARC:UPI0000175A77; UNIPARC:UPI0000175A78; UNIPARC:UPI0000175A79
C;Gonetics:
A;Introns: 88/2
C;Function:
A;Pathway: xylan degradation
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Superfamily: signal sequence #status predicted degradation
endo-1,4-beta-xylanase (EC 3.2.1.8)
N;Alternate names: xylanase
C;Species: Trichoderma harzianum
                                                                 RESULT
A44593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S71473
A;Molecule type: DNA
A;Residues: 1-241 <YOS>
A;Cross-references: UNIPROT:Q12580; UNIPARC:UPI00000421AB; EMBL:D49851; NID:g1339859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Chaecomium gracile
C;Date: 09-Dec-1997 #sequence_revis:
C;Accession: S71473; S78207
R;Yoshino, S.; Oishi, M.; Moriyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S71473
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A;Title: Two family G xylanase genes from Chaetomium gracile A;Reference number: S71472; MUID:96118924; PMID:8595661
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F;116,207/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Chaetomium gracile;Date: 09-Dec-1997 #text_change 09-Jul-2004;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004;Accession: 871473; 878207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                              IHPEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTTPNSE-GWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARA
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                                                                                                                                                                                                                                                                                          TTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                QTLTSSQTGTNNGYYYSFWTDGQGNVQYTNEAGGQYSVTWSGNGNWVGGKGWNPG-SART
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                                                                                                                                                                                                                                                                                                                                         INYTANYNPNGNSYLAVYGWTRNPLIBYYVVENFGTYNPSTGATRLGSVTTDGSCYDIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : endo-1,4-beta-xylanase B #status predicted
endo-1,4-beta-xylanase homology <XYL>
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; Pred. No. 2.9e-45;
27; Mismatches 43;
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                                              [validated] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.; Tsukagoshi,
                                            fungus (Trichoderma harzianum)
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QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60

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C;Date: 27-Ju
C;Accession:
R;Yaguchi, M.
                                                                      F;86,177/Active site: Glu #status predicted
F;126-127/Cleavage site: Pro-Ser (unidentified proteinase)
F;129-130/Cleavage site: Glu-Gly (unidentified proteinase)
                                                                                                                          A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
E;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-190 <YAG>
                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: xylanase IIB
C;Species: Trichoderma viride
C;Date: 27-Jun-1994 #sequence_revision
C;Accession: A44595
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C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F;86,177/Active site: Glu #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain E58
R;Campbell, R.L.; Rose, D.R.
submitted to the Brookhaven Protein Data Bank,
A;Reference number: A52868; PDB:1XND
                                                                                                                                                                                                                          A;Cross-references:
C;Function:
                                                                                                                                                                                                                                                                                                                                                            R;Yaguchi, M. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     endo-1,4-beta-xylanase (EC 3.2.1.8)
N;Alternate names: xylanase IIB
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A;Cross-references: UNIPARC:UPI00000493CB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: A44593
                                                                                                                                                                                                        A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic
                                                                                                                                                                                                                                                                                                                         A; Accession: A44595
                                                                                                                                                                                                                                                                                                                                        A:Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
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                   Query Match
Best Local :
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; Pred. No. 6.9e-45
27; Mismatches 4:
27;
                   Score
Pred.
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               636.5; DB 1
No. 6.9e-45;
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A; Cross-references:
                                                     A,Title: Cloning, sequencing and enhanced expression of A,Reference number: S39883; MUID:94088442; PMID:8264524 A,Accession: S39883
                                                                                                                                N;Alternate names: endoxylanase II
C;Species: Trichoderma reesei
C;Date: 19-Mar-197 #sequence_revis
C;Accession: S39883; S39884
                                                                                                                                                                                           RESULT 9
$39883
endo-1,4-beta-xylanase (EC 3.2.1.8)
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A;Title: The two major xylanases from trichoderma reesel: character:
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                      A; Molecule type: DNA
A; Residues: 1-223 <SAA>
                                                                                                   R;Saarelainen, R; Paloheimo, M; Fagerstroem, Mol. Gen. Genet. 241, 497-503, 1993
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A; Residues: 1-222 < TOE>
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                                                                                                                                Date: 19-Mar-1997 #sequence_revision 19-Mar-1997;Accession: S39883; S39884
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                                                                                                                                                                                                                                                                                                                                                                  121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                                                                                                                                                                                                 93
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                                                                                                                                                                                                                                                                                                                                                                                                                              HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTIQPGTGYNNGYFYSYWNDGHGGVTYTNGPGGQPSVNWSNSGNFVGGKGWQPGTKNKVI
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         UNIPROT:Q02244; UNIPARC:UPI00000421A8; EMBL:S67387; NID:g455906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 635.5; DB 2
Pred. No. 9.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from trichoderma reesei: characterization of both enzyments
                                                                                                                                                                                             II precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                  R.; Suominen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                              #text_change 09-Jul-2004
                                                                                                                                                                                               fungus (Trichoderma reesei)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: X69573; NID: g396563;
                                                                                      Trichoderma reesei
                                                                                                                  P.L.; Nevalainen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
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A; Pathway: xylan degradation C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degrae F;1-19/Domain: signal sequence #status predicted <SIG>F;20-33/Domain: propeptide #status predicted <PRO>F;34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>F;45-223/Domain: endo-1,4-beta-xylanase homology <XYL>F;45-223/Domain: endo-1,4-beta-xylanase homology <XYL>F;10,94/Binding site: substrate (Tyr) #status predicted F;110,121/Binding site: substrate (Tyr) #status predicted F;119,210/Active site: Glu #status predicted
                                                                                                                                                                                C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;12-190/Domain: endo-1,4-beta-xylanase homology <XYI>F;77,88/Binding site: substrate (Tyr) #steatus predicted F;86,177/Active site: Glu #status predicted
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A;Experimental source: strain QM6a
A;Accession: S3984
A;Molecule type: protein
A;Residues: 34-43;49-57;121-151;178-191 <SAF>
A;Residues: 34-43;49-57;121-151;178-191 <SAF>
A;Cross-references: UNIPARC:UPI0000175A7C; UNIPARC:UPI0000175A7D; UNIPARC:UPI0000175A7E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: xylanase
C;Species: Trichoderma virio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns:
C; Function:
                                                                                                                                                                                                                                                                           A; Pathway: xylan degradation C; Superfamily: endo-1, 4-beta-xylanase homology
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-190 < YAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: A44594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence A; Reference number: A44593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endo-1,4-beta-xylanase (EC 3.2.1.8) IIA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: xln2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in
                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: Q7M519; UNIPARC: UPI0000034D34
                                                                                                                                                                                                                                                                                                                                                 ;Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Accession:
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                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Trichoderma viride
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                                                                                           Matches
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115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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QTIGPGTGFNNGYFYSYWNDGHGGVTYTNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVI
                                           QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                                           Conservative
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                                                                                                               Score 634.5; DB Pred. No. 1e-44;
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Pred. No. 1e-44;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database,
                                                                                           Mismatches
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                                                                                                                                    DB 1;
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Biosci. Biotechnol. Biochem. 64, 2738, 2000

A,Title: Molecular cloning, overexpression, and purification of a major xyla A,Reference number: JC7577; MUID: 21077500; PMID:11210150

A,Recession: JC7577; MUID: 21077500; PMID:11210150

A,Recession: JC7577; MUID: 21077500; PMID:11210150

A,Residues: 1-212 <KIM>
A,Residues: 1-212 <KIM>
A,Cross-references: UNIPROT:Q9HPA4; UNIPARC:UPI0000069976; DDBJ:AB044941

A,Experimental source: strain KBN616

A,Recession: PC7120

A,Wolecule type: protein
A,Residues: 45-64 <KI2>
A,Cross-references: UNIPARC:UPI0000175A84

C,Comment: This enzyme has strong similarity to other fungal family 11 endox of the content o
N/Alternate names: xylanase 2
(/Species: Emericalla nidulans, Aspergillus nidulans
C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S57469
R/Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A/Description: Expression in Saccharomyces cerevisiae of two xylanase encoding A/Reference number: S57469
A/Accession: S57469
                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
S57469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: xynG2
A;Introns: 100/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita,
                                                                                                                                                                                                                                                                                           endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans
N;Alternate names: xylanase 2
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N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme has strong similarity to other fungal family 11 endoxylanases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 625; DB 2;
Pred. No. 7.5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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3 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF | | | | | | | | | | | | | | | | : : :

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C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide F;1-40/Domain: signal sequence #status predicted <SIO> F;41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT> F;54-230/Domain: endo-1,4-beta-xylanase homology <XYL> F;127,217/Active site: Glu #status predicted
                                                                                                                                                                                                                                          A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans A;Pathway: xylan degradation C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
                                                                                                                                                                                                                                                                                                                            A;Gene: xlnB
C;Function:
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 41-71 < SH2> A; Cross-references: UNIP? C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Shareck, F.; R
Gene 107, 75-82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: xylanase B
C;Species: Streptonate lividans
C;Date: 10-Mar-1994 #sequence revision 22-Nov-1996 #text_change 26-Feb-1999
C;Accession: J80590; P80239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in A,Pathway: xylan degradation C,Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology C,Keywords: glycosidase; hydrolase; polysaccharide degradation F,11-19/Domain: signal sequence #status predicted <SIG> F;19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT> F;44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
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A;Cross-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:g870834; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: I
A: Residues: 1-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000017296A; GB:M64552
A;Accession: PS0239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-333 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: JS0589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Sequences of three
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C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JS0590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;117,208/Active site: Glu #status predicted
  Matches
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     106;
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                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSGSFIPSGNGYLSVYGWTQNPLIEYYIVESYGDYNPGTAGTHQGTLESDGSTYDIYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSTPSSTGTSGGYYYSFWTDGGGDVTYTNGDGGSYTVEWTKVGNFVGGKGWNPG-SSQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roy, C
2, 1991
                                                                                                                                                                                                                                                                                             catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
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                                                                                                                                                                                                                                                                                                                                                                                                             UNIPARC: UPI000017296B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Yaguchi, M.; Morosoli, R.; Kluepfel,
                           52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 615; DB 1; 58.1%; Pred. No. 4.6e-43; tive 31; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes specifying xylanases in Streptomyees lividans MUID:92077439; PMID:1743521
                              Score
Pred.
     Mismatches
3 571.5; DB 1;
. No. 2.6e-39;
ismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces lividans
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endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp.
N;Alternate names: endo-1,3-beta-xylanase; xylanase
C;Species: Penicillium sp.
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7307; PC7066
R;Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A;Title: Purification, characterization, and molecular cloning of acidophili A;Reference number: JC7307
A;Molecular type: DNA
A;Residues: 1-221 <KIM-
A;Cross-references: UNIPROT:Q9UUQ2; UNIPARC:UPT00000421AD; DDBJ:AB035540
                                                                                                                                                                                                                                                                                                               RESULT 15
JC7307
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A;Cross-references: UNIPROT:Q9RKN6;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T50601
R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, Mol. Microbiol. 21, 77-96, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb
A;Reference number: Z20556; MUID:97000351; PMID:8843436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor N,Alternate names: xylanase B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: xlnB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Streptomyces coelicolor
|Spate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004|
|Spate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGYARITVADVG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSPNPSGNAYLALYGWTSNPLVBYYIVDNWGTYRPTGEYK--GTVTSDGGTYDIYKTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF 62
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                                                                                                                            molecular cloning of acidophilic xylanase
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A;Accession: PC7086
A;Molecule type: protein
A;Residues: 32-51 <KI2>
A;Cross-references: UNIPARC:UPI0000175A85
C;Genetics:
C;Genetics:
A;Gene: xynA
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C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: glycoprotein; glycosidase; hydrolase
Search completed: February 10, 2006, 15:02:21 Job time: 25.0764 secs
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Matches 103
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                                                                      YESSGSSTITVS
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Conservative 37;
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Pred. No. 3.3e-38;
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: uniprot_sprot:*
2: uniprot_trembl:*
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first 45 summaries
  GenCore version (c) 1993 - 2006
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O13447 COCSA
Q70T28 9PLEO
Q7SDQ1 NEUCR
Q4WG11 ASPFU
                                                    XYNA EMENI
Q58767 EMENI
Q059767 EMENI
Q0050 COCCA
Q9HGE1 HUMGT
XYN1 HUMIN
Q12580 9PEZI
Q811V6 9PEZI
Q811V6 9PEZI
Q7M520 TRIVI
XYN2 TRIRE
Q02244 TRIRE
Q02244 TRIRE
Q07519 TRIVI
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Q51SA1 MAGGR
Q51SA1 MAGGR
Q92245 MAGGR
Q766V1 9ASCO
XYNA SCHCO
              Q8J1V5_9PEZI
Q6UN40_9PEZI
XYN_TRÏHA
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XYNA_PAEVA
Q9UVZ3_9PLEO
Q9C1R2_FUSOX
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 Q4WEV2_ASPFU
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Q9uvz3
Q9uvz3
Q065162
Q06263
Q51881
Q952845
Q766v1
P35879
Q125879
Q125879
Q1013447
Q770t28
Q770t28
Q790t28
Q79
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P81536
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                                                                                                                                                                                                                                                                                  5 magnaporthe
1 scytalidium
9 schizophyll
              5 chaetomium
0 chaetomium
3 trichoderma
                                                                                                                                 7 aspergillus
0 cochliobolu
1 humicola gr
4 humicola in
                                                                                                                       chaetomium
                                                                                                                                                                                        neurospora
emericella
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aspergillus
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setosphaeri
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fusarium ox
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	
609	615	616	617	617	617	619	619	620	621	623.5	625	627.5	629.5	
56.0	56.5	56.6	56.7	56.7	56.7	56.9	56.9	57.0	57.1	57.3	57.4	57.7	57.9	
233	221	225	231	225	225	231	231	221	225	223	232	223	220	
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XYN2_MAGGR	XYNB_EMENI	XYN2_ASPNG	Q9C1R1_FUSOX	Q6QA21_9EURO	Q8TG22_ASPNG	Q7ZA57_GIBZE	Q4HVK9_GIBZE	Q5AQR5_EMENI	XYNB_ASPKA	Q99015_TRIRE	Q9HFA4_ASPOR	Q7Z8Q3_TRIVI	Q8J0T4_9HYPO	
PS5335	P55333	P55330		Q6qa21	Q8tg22	Q7za57		Q5aqr5	P48824	Q99015	Q9hfa4	Q7z8q3	Q8j0t4	
magnaporthe	emericella	aspergillus	fusarium ox	aspergillus	aspergillus	gibberella	gibberella	aspergillus	aspergillus	trichoderma	aspergillus	trichoderma	trichoderma	

THELA

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RESULT 1

XYNA THEE

ID XYNA
AC 0430

DT 15-1

DT 25-1

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043097;
15-DEC-1998
15-DEC-1998
13-SEP-2005
EMBL; U35436; AAB94633.1; -; Genomic_DNA.
pDB; IYNA; X-ray; @=32-225.
InterPro; IPR001137; Glyco_hydro_11.
pfam; pF00457; Glyco_hydro_11; 1.
pRINTS; pR00911; GLHYDRLASE11.
pROSITE; pS007776; GLYCOSYL_HYDROL_F11_1; 1.
pROSITE; pS00777; GLYCOSYL_HYDROL_F11_2; 1.
3D-structure; Glycosidase; Hydrolase; Pyrrolidone signal; Xylan degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Thermophilic xylanase from Thermomyces x-ray structure and modeling studies."; Biochemistry 37:13475-13485(199).
-I- CATALYTIC ACTIVITY: Endohydrolysis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
STRAIN=DSM 5826 / Tsiklinsky;
MEDLINE=98426042; Pubmed=9753433; DOI=10.1021/bi9808641;
Gruber K., Klintschar G., Hayn M., Schlacher A., Steiner Kratky C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97033440; PubMed=8879171; DOI=10.1016/0168-1656(96)01516-7; Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.; "Cloning and characterization of the gene for the thermostable xylanase XynA from Thermomyces lanuginosus."; J. Biotechnol. 49:211-218(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermomyces lanuginosus (Humicola lanuginosa).
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota;
NCBI_TaxID=5541;
                                                                                                                                                                                                                                                                                                                removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN=DSM 5826 / Tsiklinsky;
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PATHWAY: Xylan degradation.
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linkages in xylans.
BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temperature dependence:
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RESULT 2
XYNA PAEVA
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AC P81536;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence updat
DT 10-MAY-2005 (Rel. 47, Last annotation upo
DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xyla
DE xylanohydrolase) (PVX).
OS Paecilomyces variotii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycot
C Eurotiales; Trichocomaceae; mitosporic Tr
OX NCBI TaxID=45996;
RN [1]
RP AND 123-128.
RC STRAIN=Bainier;
RC STRAIN=Bainier;
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    MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348; Kumar P.R., Eswartamoorthy S., Vithayathil P.J., Viswamitra M.A. "The tertiary structure at 1.59 A resolution and the proposed a acid sequence of a family-11 xylanase from the thermophilic fun
                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces
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Proton donor.
Pyrrolidone carboxylic
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Pred. No. 7.3e-87;
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PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.

PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.

3D-structure; Acetylation; Direct protein se Hydrolase; Xylan degradation.

ACT_SITE 86 86 Nucleophile (By ACT_SITE 178 178 Proton donor (BY ACT_SITE 178 PR
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J. MOl. Biol. 295:581-593(2000).
-I- CATALYTIC ACTIVITY: Endohydrolysis
linkages in xylans.
-I- BIOPHYSICOCHEMICAL PROPERTIES:
Degefu Y., Paulin L., Lubeck P.S.;
"Cloning, sequencing and expression of a x
pathogen Helminthosporium turcicum Pass.";
Eux. J. Plant Pathol. 107:457-465(2001).
EMBL; AJ238895; CAB52417.1; -; Genomic_DNA
                                                                                                                                                                                                                  Setosphaeria turcica.
Eukaryota; Fungi; Ascomycota;
Pleosporales; Pleosporaceae;
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InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
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SIMILARITY: Belongs to the glycosyl
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DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;
DR GO; GO:004553; F:carbohydrate metabolism; IEA.
DR GO; GO:0045493; F:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco hydro_11; 1.
DR PRINTS; PR0091; GLYCOSYL HYDROL F11 1; 1.
DR PROSITE; P800776; GLYCOSYL HYDROL F11 1; 1.
DR PROSITE; P800777; GLYCOSYL HYDROL F11 2; 1.
KW Signal; Xylan degradation.
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Best Local S
Matches 136
                                                                                                                HSSP; 043097; IVNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-9
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0045493; P:xylan catabolism; IEA.
InterPro, IPR001137; Glyco hydro 11.
Pfam; PP00457; Glyco hydro 11.
PRINTS; PR00911; GLHYDRLASE11
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
RPCSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC6.
Query Match
Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9C1R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.

MEDLINE=21654148; PubMed=11795847; DOI=10.1007/800294-001-0260-0;

MEDLINE=21654148; Roncero M.I.G., Di Pietro A., Hera C.;

Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;

"Molecular characterization of a novel endo-beta-1,4-xylanase gen-
"molecular characterization of a novel endo-beta-1,4-xylanase gen-
trom the vascular wilt fungus Fusarium oxysporum.";

from the vascular wilt fungus Fusarium oxysporum.";

Curr. Genet. 40:268-275(2001).

EMBL; AP246830; AAK27974.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Aacomycota; Pe
Hypocreomycetidae; Hypocreales;
Fusarium oxysporum complex.
NCBI_TaxID=59765;
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01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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227 AA;
   Conservative
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71.6%;
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ota; Pezizomycotina; Sordariomycetes;
eales; mitosporic Hypocreales; Fusari
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Score 750; DB
Pred. No. 3.2e
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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Pred. No. 4.7e-58;
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                                  DB 2;
.2e-57;
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                                                             Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 227
                                                                                                                                 CRC64;
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Holden F.R., Walton J.D.;

#Xylanases from the fungal maize pathogen Cochliobolus

"Xylanases from the fungal maize pathogen Cochliobolus

"Xylanases from the fungal maize pathogen Cochliobolus

"Xylanases from the fungal maize pathogen Contributes

-i- FUNCTION: Major xylan-degrading enzyme. Contributes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XYN1_CO
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01-FEB-1995 (Rel. 31, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Endo-1,4-beta-xylanase I precursor (EC 3.2.)
beta-yylan xylanohydrolase 1).
                                         InterPro; IFR001137; Glyco hydro 11.
Pfam; PF00457; Glyco hydro 11; 1-
PRINTS; PR00911; GLYCOSIL HYDROL F11 1;
PROSITE; PS00776; GLYCOSYL HYDROL F11 1;
PROSITE; PS00777; GLYCOSYL HYDROL F11 2;
Direct protein sequencing; Glycosidase; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Race 1 / Isolate SB111;
MEDLINE=94003417; PubMed=8400376;
Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
Papel P.C., Panaccione disruption of XYL1, a beta
"Cloning and targeted gene disruption of XYL1, a beta
gene from the maize pathogen Cochliobolus carbonum.";
Mol. Plant Microbe Interact. 6:467-473(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cochliobolus carbonum (Bipolaris zeicola).
Bukaryota; Fungi; Ascomycota; Pezizomycoti
Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCCA
                                                                                                                                                                                           SMR; Q06562;
                                                                                                                                                                                                              EMBL; L13596; AAA33024.1;
HSSP; O43097; 1YNA.
                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=XYL1;
                                                                                                                                                                                                                                                                                      removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 inkages in xylans.
1 PATHWAY: Xylan degradation.
1 PATHWAY: Xylan degradation.
1 SUBCELLULAR LOCATION: Secreted.
1 PTM: The N-terminus is blocked.
                                                                                                                                                                                                                                                                                                          as long as its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                walls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collin Molecular cloning and DNA sequencing of a xylanase phytopathogenic fungus Ascochyta pisi Lib."; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databa EMBL; 268891; CAA93120.1; -; Genomic_DNA. HSSP; 043097; 1YNA.
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SIGNAL
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; Pred. No. 1.1e-56;
22; Mismatches 33
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Nucleophile (By similarity).
Proton donor (By similarity).
W -> I (in Ref. 2).
G -> A (in Ref. 2).
S -> W (in Ref. 2).
S -> W (in Ref. 2).
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                                                                                                                                                                              Score 721; DB 2;
Pred. No. 7.9e-55;
                                                                                                                                                                                                                                                                                            Potential.
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                                                                                                                                                                                                                                           RA Alt-Zahra M. Allen N. Allen T., An P. Anderson M. Anderson S. A Atzachchi H., Armbruster J. Bachantsang P., Baldwin J., Barry A., Ra Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A., Ra Bayul T., Blitshsteyn B., Bloom T., Blye J., Bagularwsky L., Ra Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., Calivo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M., Ra Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M., Ra Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C., Ra Dorjee K., Davris L., Duffey N., Dupes A., Elkins T., Engels R., Ra Erickson J., Farins A., Faro S., Ferreira P., Fischer H., Ra Fickson J., Farins A., Faro S., Ferreira P., Fischer H., Ra Fickson J., Farins A., Faro S., Ferreira P., Fischer H., Ra Honan T., Horn A., Houde N., Highes L., Hume W., Hugbts K., Hiev I., Arangos B., Hall J., Hatcher B., Heller A., Higgins H., Ra Honan T., Horn A., Houde N., Highes L., Hume W., Husby E., Iliev I., Ra Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang T., Lokyitsang T., Lowis T., Lucien O., Landers T., Leger J., Levine S., Lewis D., Lewis T., Lucien O., Marabella R., Maru K., Matthews C., Mauceli E., Mandordon J., Marabella R., Maru K., Matthews C., Mauceli E., Ra Mcarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L., Mozbu C., Mozbu N., O'donnell P., Okoawo O., Porleary S., Comotosho B., Piqani B., Parker S., Perrin D., Phunkhang P., Piqani B., Rotta R., Richardson S., Rase C., Rodriguez J., Rogers J., Rogov P., Ra Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T., Piqani B., Sherjaa N., Shi J., Smirnov S., Smith C., Soughez C., Rander E., Stone S., Stubbs M., Talamas J., Tchuinga P., Ra Yenkaraman V., Vinson J., Wilkinson J., When B. J., Topham K., Tander E., Stone S., Stubbs M., Talamas J., Tchuinga P., Rander E., Mander E., Stubes M., Talamas J., Topham K., Tander E., Stubes M., Talamas J., Topham K., Tander E., Stubes M., Talamas J., Topham K., Tander E., Stubes M., Talamas J., Topham K., Stander E., Stub
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13-SEP-2005
13-SEP-2005
                           STRAIN=70-15;
Dean R., Mitchell T.,
Submitted (OCT-2003)
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Sordariomycetes incertae sedi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames=MG08424.4;
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                                                                                                                                                                                                                               Zimmer A., Zody M., Lander E.;
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Last annotation update)
                              D., Pan H., Thon N
EMBL/GenBank/DDBJ
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Hafez N.,
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RESULT 8
Q92245 MAGGR PRELIMINARY;
ID 2045245 AGGR PRELIMINARY;
AC Q92245;
DT 01-FEB-1997 (TrEMBLrel 02,
DT 01-FEB-1997 (TrEMBLrel 25,
DE Endo-beta-1,4-D-xylanase.
GN Magnaporthe grisea (Rice bl
OC Endo-well Fungi; Ascomycot
OC Sordariomycetes incertae se
OX NCBL_TAXID=148305;
RN MUCLEOTIDE SEQUENCE.
RC TIGSUE-Mycelium;
RA WLS.-C., Darvill A.G., Alb
RA GO; GO:0004553; F:hydrolase
DR EMBL; AX144349; AAB06573.2;
DR HSSP; O43097; IYNA.
DR GO; GO:0004553; F:carbohydre
DR GO; GO:0004553; F:hydrolase
DR GO; GO:004553; F:hydrolase
DR GO; GO:004553; Glyco-hydro
DR Pfam; PF00457; Glyco-hydro
DR Pfam; PF00457; Glyco-hydro
DR PRINTS; PR00911; GLIYDRLASE
DR PROSITE; PS00776; GLYCOSYL-
DR PROSITE; PS00776; GLYCOSYL-
DR PROSITE; PS00777; GLYCO-Nydro
DR PROSITE; PS00777; GLYCO-Nydro
DR PROSITE; PS00777; GLYCOSYL-
DR PROSITE; PS00777; GLYCO-Nydro
DR PROSITE; PS00777; GLYCOSYL-
DR PROSITE; PS00777; GLYCOSYL-
DR SEQUENCE 231 AA; 25305 M
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Best Local S
Matches 125
                                                                                                                                                                 A Wu S.-C., Darwill A.G., Albersheim P.;

A Wu S.-C., Darwill A.G., Albersheim P.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AX144349; AAB06573.2; -; Genomic_DNA.

R HSSP; 043097; 1NNA.

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosy GO:0005975; P:carbohydrae metabolism; IEA.

R GO; GO:0004593; P:cylan catabolism; IEA.

R GO; GO:0045493; P:xylan catabolism; IEA.

R GO; GO:0045493; P:xylan catabolism; IEA.

R GO; GO:0045493; P:xylan catabolism; IEA.

R FO; GO:0045493; P:xylan catabolism; IEA.

R FROSITS; PRO091137; Glyco_hydro_11.

R PROSITS; PR0091137; GLYCOSYL_HYDROL_F11_1; 1.

R PROSITS; PS007776; GLYCOSYL_HYDROL_F11_2; 1.
Query Match
Best Local Similarity 66:
Matches 125; Conservative
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EMBL; AACUO1001255; EAA49509.1; -; Genomic_DNA.

InterPro; IPR002453; Beta_tubulin.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PROSITE; PR00911; GLHYDRLASE11.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. NCBI_TaxID=148305;
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01-FEB-1997 (TrEMBLrel. 02,
01-OCT-2003 (TrEMBLrel. 25,
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Submitted (OCT-2003) to
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EMBL/GenBank/DDBJ whole
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Score 705; DB 2
Pred. No. 2e-53;
5; Mismatches
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Pred. No. 1.7e-53;
5; Mismatches 36
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                                                             Length 231;
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; ABB11442; BAD07040.1; -; Genomic_DNA.

R HSSP; p09850; 1BCX.

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . .

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0045493; P:xylan catabblism; IEA.

R GO; GO:0045493; P:xylan catabblism; IEA.

R InterPro, IPR001137; Glyco_hydro_11.

R PRINTS; PR00911; GLYCOSYL_HYDROL_F11_1; 1.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

W Xylan Garradation
                                                                                                                                                                                               Matches
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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V1_9ASCO
Q766V1_9
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                             Xylan degradation
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NCBI_TaxID=85995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=sxyl1;
Scytalidium thermophilum.
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                                                                                                108 SGTFNPSGNGYLAIYGWTTNPLVEYYIVENFGTYDPSSQAQNLGTFYVDGSNYKIAKSTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9ASCO
                                                                                                                                                                                                            Similarity
                                                                                                                    EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPSSTGTHDGFYYSWWTDNGAQATYTNNAGGSYSITWSGNGNLVGGKGWNPG-SARNVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANYRPNGNSYLSVYGWTRNPLVEYYVVENFGTYDPSSQASRKGTINVDGATYQVAQSTR
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                                                               VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS
                                                                                                                                               TPSSTGWHGGYFYSFWTDGGGEVNYWNGNNGNYGVNWRNCGNFVGGKGWKPGA-ARTINY
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                       SGYARITV 190
                                               YNOPSIIGTATFNOYWSVRONKRSSGSVNVGAHFQAWAQRGLNL-GNHDYQIVATEGYOS
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SGSASITV
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                                                                                                                                                                                                                                                AA,
 234
                                                                                                                                                                                                                                                25526 MW;
                                                                                                                                                                                                            61.1%; Score 665; DB 2; 63.8%; Pred. No. 6.4e-50;
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27,
27,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitosporic Ascomycota; Scytalidium.
                                                                                                                                                                                                                                                C929BE7FD73682CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                       Length 235;
                                                                                                                                                                                                 Indels
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RESULT 10
XYNA_SCHCO
ID XYNA_SCHCO
AC P35809;

STANDARD;

PRT;

197

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Query Match
Best Local S
Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
PROTEIN SEQUENCE.
STRAIN-ATCC 38548 / Delmar;
Yaguchi M., Roy C., Ujiie M., Watson D.C., Wakarchuk W
Yaguchi M., Roy C., Ujiie M., Watson D.C., Wakarchuk W
Yan' Visser J., Beldman G., Kusters-van Someren M.A.,
                                                                                                                                                                                                                                                           Direct pr
ACT_SITE
ACT_SITE
DISULFID
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STRAIN-ATCC 38548 / Delmar;
MEDLINE-94155888; PubMed-7906649;
Bray M.R., Clarke A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE, AND DISULFIDE BONDS.

STRAIN-ATCC 38548 / Delmar;
MEDLINE-94663044, PubMed-8243636; DOI=10.1016/0014-5793(93)80698-T;
Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
                                                                                                                                                                                                                                                                                                    InterPro; IPH001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Direct protein sequencing; GlycosIdase; Hydrolase; Xylan ACT_SITE 87 87 Nucleophile (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jurasek L., Paice M.G.; "Amino acid sequence and thermostability of xylanase A from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Basidiomycota; Hymenomycet
Agaricales; Schizophyllaceae; Schizophyllum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A44597; A44597.
HSSP; P81536; 1PVX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizophyllum commune
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                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
as long as its content '7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entification of a glutamate residue at the active site of xyrom Schizophyllum commune.",
. J. Biochem. 219:821-827(1994).
FUNCTION: Hydrolyzes xylans into xylobiose and xylose.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Active over a very broad pH range; PATHMAY: Xylan degradation. SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linkages in xylans.
BIOPHYSICOCHEMICAL PROPERTIES:
    62
                                                                                                                                                                 Similarity
                                                                                            TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 61
FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121
                                                TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS
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                                                                                                                                           Conservative
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Belongs to the glycosyl hydrolase 11 (cellulase
                                                                                                                                                                                                                                                             184
160
                                                                                                                                                                                                                                       20979 MW;
                                                                                                                                                                 60.9%; Score 663; DB 1; 61.3%; Pred. No. 7.7e-50;
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Last annotation update)
A (EC 3.2.1.8) (Xylanase
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idiomycota; Hymenomycetes;
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                                                                                                                                                                                                                                                                                   similarity)
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79 9PEZI
Q12579_
                                                                                                                                                                                                                                                            GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:004543; P:xylan catabolism; IEA.
GO; GO:004543; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYOROYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Glycosidase; Hydrolase; Xylan degradation.
SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.

MEDLINS=96118924; PubMed=8595661; DOI=10.1007/BF00313196;

MEDLINS=96118924; PubMed=8595661; DOI=10.1007/BF00313196;

Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;

"Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans.";

Curr. Genet. 29:73-80(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases. EMBL; D49850; BAA08649.1; -; Genomic_DNA. PIR; S71472; S71472.
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Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
NCBI_TaxID=47794;
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SGSSSITVS 219
                         SGYARITVA 191
                                                  VNQPSIEGTSTFDQFWSVRQNHRSSGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQS
                                                                                                       SGTFSPQGNGYLAIYGWTQNPLVEYYIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTR
                                                                                                                                                          TPSGTGTNNGYFYSFWTDGGGTVNYQNGAGGSYSVQWQNCGNFVGGKGWNPGA-ARTINF
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Pred. No. 3.6e-49;
B; Mismatches 42
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Q70T28;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                    NUCLEOTIDE SEQUENCE.

PubMed=15016446; DOI=10.1016/j.biochi.2004.01.001;

Degefu Y., Lohtander K., Paulin L.G.;

"Expression patterns and phylogenetic analysis of (htxyl 1 and htxyl 2) from Helminthosporium turcicu leaf blight of maize.";

Biochimie 86:83-90(2004).
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EMBL; AJ004802; CAA06151.1; -;
HSSP; QBJ1V6; 1H1A.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
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Best Local S
Matches 115
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GO; GO:0004553
GO; GO:0005975
GO; GO:0045493
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01-MAR-2004 (TrEMBLrel. 26, Last sequence up
01-FBB-2005 (TrEMBLrel. 29, Last annotation
Hypothetical protein (Probable endo-1, 4-bet
Name=NCU0285.1; Synonyms=B10D6.120;
                           Schulte U.
Nyakatura
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5141;
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Sordariomycetidae; Sordariales
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Q7SDQ1;
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231 AA;
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              Aign V., Hoheisel J., Brandt P.,
L., Mewes H.W., Mannhaupt G.;
NOV-2003) to the EMBL/GenBank/DDB
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                 EMBL/GenBank/DDBJ
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Pred. No.
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              Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
A Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
A Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
A Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
A Fosker N., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
A Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
A Haas H., Harris D., Horluchi H., Huang J., Humphrey S., Jimenez J.,
A Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
A Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
A Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
A Keller N., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
A Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
A Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
A Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
A Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
A Ronning C.M., Rutter S., Sandres R., Smares R., Smares R.
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ABBERGIIIUB fumiglatus Af293.
Eukaryota; Fungi; ABcomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; ABcomycota; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Endo-1,4-beta-xylanase (XlnA), putative.
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EMBL; AABX01000046; E
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=330879;
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BX842624; CAE76228.1; -; Genomic_DNA.
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     Saunders D.,
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Pred. No. 9.8e-49;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J. White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W., "Genomic sequence of the pathogenic and allergenic filamentous fungus
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Xylan
                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
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degradation.
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                                                                                                                                                                                                                                                     3 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                             VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS
                                                                                 SGYARITY 190
                                                                                                              YNAPSIEGTKTFTQYWSVRTSKRTGGTVTMANHFNAWSRLGMNL-GTHNYQIVATEGYQS
                                                                                                                                                                    GGSFNPSGNGYLAVYGWTTNPLIEYYVVESYGTYNPGSGGTFRGTVNTDGGTYNIYTAVR
                                                                                                                                                                                             EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR
                                                                                                                                                                                                                          TPSSTGWNNGYYYSFWTDGGGDVTYTNGAGGSYSVNWRNVGNFVGGKGWNPG-SARTINY
                                                      SGSASITV
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             10,
              2006,
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Pred. No. 1e-48;
6; Mismatches
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              15:01:23
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completed: February ne : 196.852 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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and is der
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                  1088
1088
1083
965
742
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663
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Match
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1088
1 QTTPNSEGWHDGYYYSWWSFN
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
    QTTPNSEGWHDGYYYSWWSD......VATEGYFSSGYARITVADVG
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    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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             US-08-886-765-2
US-09-115-660-2
US-09-570-8568-23
US-09-570-8568-23
US-09-570-8568-29
US-08-044-621D-29
US-08-044-621D-28
US-08-044-621D-28
US-08-044-621D-26
US-08-044-621D-27
US-09-947-370-17
US-09-942-14
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Sequence 2, Appli
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Sequence 17, Appli
Sequence 20, Appli
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B &	Query Best 1 Matche	SS -	, ., ., ., ., .,	, ,, ,, ,, ,, ,, ,, ,, ,, ,,		RESULT US-08-: ; Seque ; Pate; GEN	ממטטטטטטטטממממ
1 QTTPNSEGWHDGY 32 QTTPNSEGWHDGY	Match Local Similarity es 194; Conservat	TELEPHONE: TELEPAX: 2 TELEPAX: 2 FORMATION FOR SEQUENCE CHAR LENGTH: 22 TYPE: amin TOPOLOGY: MOLECULE TYPE -886-765-2	LASSIFICAT ORNEY/AGEN ORNEY/AGEN AME: Lamb EGISTRATIO EFERENCE/D ECOMMUNICA	ZIP: 1074 ZIP: 10174 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatib OPERATING SYSTEM: DOS SOPTWARE: FastSEQ for CURRENT APPLICATION NUMBER: US PILING DATE: US	APPLICANT: Walgner, Pet APPLICANT: Wallertz, A APPLICANT: Wallertz, A APPLICANT: Knap, Inge TITLE OF INVENTION: An NUMBER OP SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: NO. 58175 STREET: 405 Lexingto CITY: New York	1 1866-765-2 1866-765-2 180	88 630.5 58.0 190 80 621 57.1 225 80 627 56.7 225 80 86.5 53.9 226 81 574.5 52.8 296 8574.5 52.8 296 8574.5 52.8 296 877.5 52.8 296 877.5 52.6 231 877.5 52.5 215 877.7 52.5 215 877.5 52.5 215 877.5 52.5 215 877.5 52.5 215 877.5 52.
TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARA 	100.0%; Score 1088; DB 1; 100.0%; Pred. No. 4e-97; ive 0; Mismatches 0;	12-86/-0123 12-878-9655 SEQ ID NO: 2: ACTERISTICS: 5 amino acids o acid linear linear	TION:	RM: stte stte stte strible str	ner, Heter lertz, Anette ip, Inge Helmer ITON: Animal Feed Additives NCES: 2 ADDRESS: ADDRESS: No. 58175000 No. 5817500disk of No. Lexington Avenue	ALIGNMENTS . US/08886765 Peter Kamp	2 US- 2 US- 2 US- 2 US- 2 US- 2 US- 2 US- 1 US-
DGGNLVGGKGWNPGLNARAI 60 DGGNLVGGKGWNPGLNARAI 91	Length 225; Indels 0; Gaps 0				5817500th America, Inc.		Sequence 22, Appl Sequence 26, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 16, Appli Sequence 17, Appli Sequence 13, Appl Sequence 10, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl

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SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino
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Patent No. 6245546
                                                                                                                                                                                 Matches
                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: I
APPLICANT: I
APPLICANT: I
APPLICANT: I
                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 405 Lexington Avenue CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONCERNING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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 152
                 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                                                             61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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                                                                                                                     QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                      QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
                                                            HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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                                                                                                                                                                              Score 1088; DB 2;
Pred. No. 4e-97;
; Mismatches 0;
                                                                                                                                                                                                            Length 225;
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RESULT 4
US-09-570-856B-23
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US-09-570-856B-23
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                                                                     PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOPTWARE: Patentin version 3.1
SEQ ID NO 23
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RF/KMS/RMK
CURRENT APPLICATION UNMEER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 194
                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09570856B Patent No. 6682923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bentzien, APPLICANT: Dahiyat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: "Xaa" at position 1 is
                                   LENGTH: 194
TYPE: PRT
                   ORGANISM: Paecilomyces variotii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
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Bassil I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1083; DB 2; Pred. No. 1e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-std-residue "PCA NH3+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Query Match

Local Similarity

DB 2; Length 194,

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PATENT NO. 6682923

GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahlyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RNS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR PILING DATE: 1999-05-12
NUMBER OF SEG ID NOS: 34
SOFTWARE: Patentin version 3.1
SEG ID NO 29
LEWTH. 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Cochliobolus carbonum US-09-570-856B-29
                                                                                                                                                                             RESULT 6
US-08-044-621D-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                     Sequence 29, Application US/08044621D Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 221
                                           APPLICANT:
                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                          181 FSSGYARITV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                             150 TRTNQPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMNL-GQHYYQIVATEGY 208
                                                                                                                                                                                                                                                                                                                                                                                                    121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SSGYARITVADVG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 TYSGTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYDPSSQSQNKGTVTSDGSSYKIAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 ONTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                                  FSTGNAQITV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGYARITVADVG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYNAPSIDGTQTPNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09570856B
Wing L. Sung
Makoto Yaguchi
Robert L. Campbell
David R. Rose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.2%; Score 742; DB 2; Length 221; 70.0%; Pred. No. 9.6e-64; tive 22; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
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Pred. No. 2.4e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
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US-08-044-621D-29
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION UNMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in.,
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Schizophyllum commune
STRAIN: Schizophyllum commune, J
INMEDIATE SOURCE:
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                               DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES I
                                                                                                                                                                                                                                                                         VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid
STRANDEDNESS: No.
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 613-563-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Ottawa
                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
KIP 1C3
                                                                                                                                                                                                                                                             1988
                                                                                         TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 61
                                                           Ontario
                                                                                                                                                                                                                                                                         Abstract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Gowling,
Suite 2600,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canada
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                       Canadian Fed. Biol.
                                                                                                                                                                                                                                                                                                                                                                 Oku T., Yaguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No No
                                                                                                                     60.9%; Score 663; DB 1; 61.3%; Pred. No. 3.4e-56; ative 26; Mismatches 43
                                                                                                                                                                                                  IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF A LOW MOLECULAR MASS XYLANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONSTRUCTION OF THERMOSTABLE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5405769 Relevant
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160 Elgin Street
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                                                                                                                                                                                                                                                                                                                                                                 Paice M., & Jurasek
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                                                                                                                                                   Length 197;
                                                                                                                         Indels
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US-08-709-912-9
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                                                                                                       US-08-709-912-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Appli
Patent No. 575984
                                Query Match
Best Local Similarity 61.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 758-298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/709,912 FILING DATE: 09-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yaguchi
APPLICANT: Ishikawa
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                     PUBLICATION INFORMATION:
AUTHORS: Oku, T
AUTHORS: Yaguchi, M
AUTHORS: Parse, M
                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELECUTATION (Z12)
                                                                                                                                                                                                                                    ORGANISM: SCHLE
ORGANISM: SCHLE
ORGANISM: SYLANASE A
THEORMATI
                                                                                                                    PAGES: Abst
DATE: 1988
                                                                                                                                                 AUTHORS: Parse, M
AUTHORS: Jurasek, L
JOURNAL: Canadian Fed.
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 277 Pa
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ER READABLE FORM:
TYPE: Floppy disk
     3 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEGYFSSGYARITY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEGYOSSGTATITV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08709912
                                                                                                                                     Abstract #676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                   197 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa Dr., Kazuhiko
VENTION: Modification of Xylanase to Improve
VENTION: Thermophilicity, Alkalophilicity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sung Dr., Wing L
Yaguchi Dr., Makoto
                                                                                                                                                                                                                                                                      Schizophyllum commune
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fitzpatric, Cella, Harper, and Scinto
                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                2) 756
, 758-2982
, 70: 9:
                                                                                                                                                                                                                                                                                                                                                                                    single
                                  60.9%; Score 663; DB 1; 61.3%; Pred. No. 3.4e-56; tive 26; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostability
                                                                                                                                                       Biol. Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039.2000
                                                                                                                                                       annual meeting
                                     43;
                                                                    Length 197;
                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sung I
                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-
TELEFAX: (212) 758-29
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 09-5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
                                                                                                                                                                 TOPOLOGY: lines
MOLECULE TYPE: p:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: IShikawa
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                 FRAGMENT TYPE: inter
ORIGINAL SOURCE:
ORGANISM: Schizoph
STRAIN: Xylanase A
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                 PUBLICATION INFORMATION:
                                                                                                                                                                                                            TYPE:
STRANDEDNESS: 81115
STRANDEDNESS: 81115
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                                                    AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
   JOURNAL:
                                AUTHORS:
                                                                   AUTHORS:
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Parse, M
Jurasek, L
Canadian Fed. Biol. Soc. annual meeting
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Yaguchi Dr., Makoto
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                                                Yaguchi, M
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RESULT 10
US-08-458-023B-4
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GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Joerg M
APPLICANT: DAhlyat, Bassil I

TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/KN9/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
Sequence 4, Application US/08458023B
Patent No. 567990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
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Best Local Similarity
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Best Local Similarity 61.3%;
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SOFTWARE: PatentIn version 3.1
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Pred. No. 3.4e-56;
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GENERAL INFORMATION:
APPLICANT: WATANABU
APPLICANT: WATANABI, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: SUMIDA, NAOMI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
APPLICANTION: REGULATORY SEQUENCE OF CELLULASE cbh1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPPIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(MMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09254733 Patent No. 6277596
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-LOSE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILLING DATE: 01-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America,
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NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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New York
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RESULT 12
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.7%; Score 638.5; DB 2; Best Local Similarity 60.2%; Pred. No. 9.4e-54; Matches 115; Conservative 27; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 223
TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: NOVEL XYLANASES,
TITLE OF INVENTION: AND USES THEREOF
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                        FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                      APPLICATION NUMBER: US 60 FILING DATE: 18-DEC-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/00 FILING DATE: 17-DEC-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                    APPLICATION NUMBER: US 60/020,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 ORVNOPSIEGTSTFYOYWSVRRTHRSSGSVNTANHFNAWASHGLTL-GTMDYOIVAVEGY 212
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                                                                                                                                                                                                                                                                                                                                                                                                           20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WASHINGTON
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LANTTO, RAIJA
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                                                                                                                                                                                            US 60/008,746
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LOCATION:
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TYPE: amino acid
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                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US 08/768,373
FILING DATE: 17-DEC-1996
                                                                                                                                                                      ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PALOHEIMO, MARJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150
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                                                                                                                                                                                                                           STATE: DC
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS
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                                                                                                                                                                                                                                                             CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                        TANTINEN, TAKUM
FAGERSTRIM, RICHARD
SUOMINEN, PIRKKO
OF INVENTION: NOVEL XYLANASES, GI
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1..261
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Pred. No. 1.4e-53;
                                                                                                                                                                                                                                                                                                                                                                 GENES ENCODING
                                                                                                                         Version #1.30
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NAME/KEY: Protein

LOCATION: 1..261
OTHER INFORMATION: /label= XLNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-242A-2
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US-08-044-621D-28
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APPLICANT: Warren |
APPLICANT: Wing L.
APPLICANT: Makoto
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/08044621D Patent No. 5405769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 113; Conservative
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
COMPUTER: IBM PC
                                                                                                                                                                                                              APPLICANT: MaKOLO YAGUCHI
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OP INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OP INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                         CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
                                                                                                                                                          STREET:
                                                                                                                                                  ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION IMFORMATION:
TELEPHONE: (202) 371-2600
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                         Wing L. Sung
                                                                                                                                                                                                                                                                                                                                                            Warren W. Wakarchuk
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PC-DOS
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; PUBLICATION DATE:
; RELEVANT RESIDUES
US-08-044-621D-28
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRAGMENT TYPE: |
ORIGINAL SOURCE:
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ANTI-SENSE: 1
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AUTHORS:
AUTHORS:
TITLE:
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                                                                                                                                                                                                                                                                                                                                                         DATE: 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Trichoderma harzianum STRAIN: Trichoderma harzianum,
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STRANDEDNESS: No.
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION:
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180
                       181 FSSGYARITVA 191
                                                     121 QRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY
                                                                               121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                            116; Conservative
                                                                                                             61 NFSGSYNPNGNSYLSIYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRT 120
                                                                                                                                                                  FSSGSASITVS 190
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F., Tan L.U.L., Senior D.J., & Saddler
J.N.
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60.7%; Pred. No. 1.2e-53;
tive 27; Mismatches 47
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RESULT 15 US-08-709-912-14

Sequence 14,

Application US/08709912

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GENERAL INFORMATION: Wing L
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Yaguchi Dr., Mazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
THERMOPHICANT TEAMORTABILITY

TARANTION: Teamostability

Talento
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
PILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-240
TELEPAX: (212) 758-240
TELEPAX: (212) 758-240
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Thrichoderma harzianum PUBLICATION INFORMATION: AUTHORS: Yaguchi, M AUTHORS: Roy, C AUTHORS: Watson, D. C. AUTHORS: Watson, D. C. AUTHORS: Tan, L. U. L. AUTHORS: Senior, D. J. AUTHORS: Senior, D. J. AUTHORS: Sediler, J. N. JOURNAL: Xylan and Xylanase PAGES: 435-438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linea:
TOPOLOGY: linea:
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
TYPE: internal
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TITLE OF INVENTION: Modification of Xylanase to Imp
TITLE OF INVENTION: Thermophilicity
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: Fitzpatric, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
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DATE: 1992
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                                                                                                                                                                              1 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
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10172-0194
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Search completed: February 10, 2006, 15:03:37 Job time : 33.8735 secs

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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US-10-237-386-24
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US-10-425-115-267585
US-10-425-115-361946
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US-10-307-441-9
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Sequence 20, Appl
Sequence 4, Appl
Sequence 2, Appli
Sequence 21, Appl
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Sequence 22, Appli
Sequence 361946,
Sequence 36, Appli
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Sequence 29, Appli
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Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 31, Appl
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			ALIGNMENTS	US-10-237-386-39	US-11-088-725A-38	US-10-307-441-10	-11	US-10-307-441-13	US-10-237-386-42	US-10-213-990-72	US-11-154-793-2	US-10-299-393-2	US-10-237-386-34	US-10-237-386-44	US-10-237-386-28	US-10-237-386-36	US-10-237-386-30	US-11-088-725A-1	US-10-213-990-66	US-10-237-386-33	-11-088-725A-4

TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity FITTE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity FILE REFERENCE: 027367-5006US CURRENT APPLICATION NUMBER: US/10/307,441 CURRENT FILING DATE: 2002-12-02 FRIOR FILING DATE: 2002-05-31 FRIOR FILING DATE: 2001-05-31 FRIOR FILING DATE: 2000-05-31 FRIOR FILING DATE: 2 RESULT 2 US-11-088-725A-46 ঠ 밁 S 밁 ঠ 문 Ś Sequence 46, Application US/11088725A Publication No. US20050214410A1 GENERAL INFORMATION: Query Match 100.0%; Score 1088; DB 4; Best Local Similarity 100.0%; Pred. No. 1.7e-97; Matches 194; Conservative 0; Mismatches 0; 181 181 1 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI FSSGYARITVADVG 194 FSSGYARITVADVG 194 QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI Indels Length 194; 0; 180 120 60 60

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09467368 Patent No. US20020160080A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
CURRENT FILING UNIVERS: US 60/556,061
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: logen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: Giroux, Genevieve R
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Kylanases Exhibiting Improved Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Q80712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  local Similarity
                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
              ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knap, Inge Helmer TITLE OF INVENTION: Animal Feed Additives NUMBER OF SEQUENCES: 2
                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                        STREET: 405 Lexington Avenue CITY: New York STATE: NY
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                                                                          APPLICATION NUMBER: US/08/886,765 FILING DATE: 1-JUL-1997
                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                   ZIP: 10174
                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
REFERENCE/DOCKET NUMBER: 4324.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600
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Mullertz, Anette
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100.0%; Pr
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Pred. No. 1.
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GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Slobesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylamse Variants Having

FILE REFERENCE: 67459-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/HB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-27
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ
US-09-467-368-2
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                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: T.
US-10-237-386-24
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 24
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Best Local :
                                                                                                                                                                                      Matches 194;
                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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92 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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                                                                                   61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
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                                                    HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                    QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                                                                                                                                  Score 1088; DB 4;
Pred. No. 2e-97;
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; TYPE: PRT
; ORGANISM: H. turcicum
US-10-237-386-21
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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           Sequence 20, Application US/10237386

Publication No. US20030180895A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PRIOR DATE: 2000-03-08
PRIOR PRIOR DATE: 2000-06-27
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Best Local Similarity
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Publication No. US20030180895A1
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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 SEQ ID NOS:
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; TYPE: PRT
; ORGANISM: C.
US-10-237-386-20
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US-10-425-115-221836
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SEQ ID NO 221836
LENGTH: 227
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SEQ ID NO 20
LENGTH: 221
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Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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215
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                                    FSSGYARITV 190
                                                                          TRINGPSIDGTRIFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMTL-GSHYYQIVATEGY
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  FSTGSASITV
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70.0%; Pri
ative 22;
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; Pred. No. 2.7e-63;
28; Mismatches 3;
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Pred. No. 8.5e-64;
2; Mismatches 33
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RESULT 9
US-10-237-386-22
Sequence 22, Appl
; Publication No. U
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A.
US-10-237-386-22
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SEQ ID NO 267585
LENGTH: 221
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Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                              SOFTWARE: P
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Best Local
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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OTHER INFORMATION: Clone ID: MRT4577_175642C.1.pep
-10-425-115-267585
                                                                                                                  PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                           APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered
FILE REFERENCE: 674509-2046
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LOCATION: (1)..(221)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                     PatentIn version 3.0
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Pred. No. 3.8e-62;
22; Mismatches 36
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GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28
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US-10-307-441-9
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Sequence 9, Application US/10307441
Publication No. US20030166236A1
GENERAL INFORMATION:
APPLICANT: SUNG, Wing L.
APPLICANT: National Research Council of Canada
APPLICANT: National Research Sylanases Exhibiting Increased Thermophilicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 361946
LENGTH: 234
TYPE: PRT
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                           EGVYQPNGNSYLAVYGWTRNPLVBYYIVENPGTYDPSSGATDLGTVECDGSIYRLGKTTR 122
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                                                                                                                                                                                                             SGYARITV 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID: MRT4577_93271C.1.pep
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Pred. No. 7.5e-61;
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TITLE OF INVENTION:

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                                                                                                                                                                                                                                                                                                  US-11-088-725A-36
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APPLICANT: White, Theresa C
APPLICANT: White, Theresa C
APPLICANT: White, Theresa C
APPLICANT: Wallace, Katie E.A.
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: 080712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.2
SEQ ID NO 36
SECOND NO 36
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PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver: 2.1
SEQ ID NO 9
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 119; Conserv
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Best Local Similarity
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CURRENT FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Schizophyllum commune
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122 RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119;
                                                               62 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121
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                                       YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 122
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                                                                                                                                                                                                        60.9%; Score 663; DB 6; 61.3%; Pred. No. 3.5e-56; tive 26; Mismatches 43
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US-10-237-386-29
Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
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; ORGANISM: S.
US-10-237-386-23
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 201
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PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
                                                                                                                                   APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
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CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR PILING DATE: 2000-03-08
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
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APPLICANT: Sibbesen, (
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No. US20030180895A1
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61.3%; Pred. No. 3.6e-56;
rative 26; Mismatches 43
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sozensen, Ole
TITLE OF INVENTION: Kylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674599-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: CT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
SEQ ID NO 26
SOPTWARE: Patentin version 3.0
SEQ ID NO 26
SEQ ID NO 26
TYPE: PRT
ORGANISM: C. Bativus
US-10-237-386-26
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; SOFTWARE: PatentIn version 3.
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-29
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US-10-237-386-26
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Publication No. US20030180895A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     Query Match 60.3%; Score 656; DB 4; Length 231; Best Local Similarity 61.1%; Pred. No. 2.1e-55; Matches 116; Conservative 27; Mismatches 45; Indels
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                                                             121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                       181 FSSGYARITV 190
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                                                                                                                                                                                                      41 OSTPSSEGYHNGYFYSWWTDGGGSAQYTMGEGSRYSVTWRNTGNFVGGKGWNPG-TGRVI 99
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                                        TRYNQPSIDGTRTFQQYWSVRQQKRVGGSVNMQNHFNAWSRYGLNL-GQHYYQIVATEGY
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Db 219 QSSGSSDIYV 228

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3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*

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; ORGANISM: H. turcicum
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/11170653 Publication No. US20050271769A1
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SOFTWARE: PA
                       APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitoz
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER: OF SEQ ID NOS: 66
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CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION STEEL 2000-06-27

NUMBER OF SEQ ID NOS: 66
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
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SEQ ID NO 22
LENGTH: 227
TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Slobesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 67459-2046

CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/11170653
Publication No. US20050271769A1
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TNQPSIDGTQTFQQYWSVRQNKRSSGSVNMKTHFDAWAAKGMKL-GTHNYQIVATEGYFS 216
                                           VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS 182
                                                                                                                                             EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR 122
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69.1%; Pred. No. 1.2e-59;
ative 22; Mismatches 34
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Sequence 29, Application US/11170653

Publication No. US20050271769Al

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
CONTRIBUTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT APPLICATION NUMBER: US/10/237,386

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR APPLICATION NUMBER: GD02-09-09

PRIOR APPLICATION NUMBER: GD02-09-09

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEO ID NOS: 66

CONTRIBED OF SEO ID NOS: 66
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Matches
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Publication No. US20050271769A1
GENERAL INFORMATION:
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ORGANISM: S.
-11-170-653-23
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CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 124
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PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
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; TYPE: PRT
; ORGANISM: C.
US-11-170-653-29
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; TYPE: PRT
; ORGANISM: C:
US-11-170-653-26
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CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                   Query Match 60.3%; Score 656; DB 7; Best Local Similarity 61.1%; Pred. No. 1.2e-53; Matches 116; Conservative 27; Mismatches 45
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Publication No. US20050271769A1
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Best Local Similarity 61.9
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitors FILS REFERENCE: 674509-2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Danisco A/S APPLICANT: Sibbesen, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB 0015751.1
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APPLICANT: Sorensen, Jens
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    160
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                                                                                       100 NYGGAFNPQGNGYLAVYGWTRNPLVEYYVIESYGTYNPSSGAQVKGSFQTDGGTYNVAVS
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                                                                                                                                 61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR
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TRYNQPSIDGTRTFQQYWSVRQQKRVGGSVNWQNHFNAWSRYGLNL-GQHYYQIVATEGY
                         TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                             SGSSSITVS 219
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61.9%; Pred. No. 1.1e-53;
7ative 28; Mismatches 42
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FSSGYARITV

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RESULT 9
US-11-170-653-27
US-11-170-653-27
; Sequence 27, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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; LENGTH: 231
; TYPE: PRT
; ORGANISM: C.
US-11-170-653-25
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CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
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                           CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
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Publication No. US20050271769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 114;
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Best Local Similarity
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Danisco A/S APPLICANT: Sibbesen, (APPLICANT: Sorensen, (APPLICANT: Sorensen, (APPLICANT: APPLICANT)
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NUMBER
                                                                                                                                                                                        TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibito: FILE REFERENCE: 674509-2046
                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                                                                                                                                                                                                                                                                                                                                                                                    OSSGSSDIYV 228
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Sorensen, Jens
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Sorensen, Jens
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NOS:
                  2000-06-27
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Pred. No. 6.7e-53;
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; TYPE: PRT
; ORGANISM: H.
US-11-170-653-27
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Best Local
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PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR PPLICATION NUMBER: PCT/IB01/00426
PRIOR PPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR PPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 35
LENGTH: 241
TYPE: PRT
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; Sequence 35, Application US/11170653
; Publication No. US20050271769A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
APPLICANT: Sorensen, Jens
TITLE OLD SORENSEN, Jens
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
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APPLICANT: Sibbesen, (
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nes 113; Conserv
                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                 1 OTTPNSE-GWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARA 59
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                                                                       TTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEG 179
                                                                                                                                     YFSSGYARITV 190
                                                                                                                                                                                                                               QTLTSSQTGTNNGYYYSFWTDGQGNVQYTNEAGGQYSVTWSGNGNWVGGKGWNPG-SART 89
                                             TORVNOPSIEGTSTFYOFWSVRONKRSGGSVNMAAHFNAWAAAGLOL-GTHDYQIVATEG 208
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                                                                                                                                                                                                                                                                                                                                             59.1%; Score 642.5; DB 7 61.8%; Pred. No. 2.2e-52;
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                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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Sequence 32, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
CURRENT SIBBESE Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

FULS REFERENCE: 674509-2046

FULS REFERENCE: 104509-2046

FULS REFERENCE: 2005-06-23

FRIOR APPLICATION NUMBER: US/11/170,653

FRIOR APPLICATION NUMBER: US/10/237,386

PRIOR APPLICATION NUMBER: CT/1B01/00426

PRIOR APPLICATION NUMBER: GENOUSS85.5

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER: GB 0015751.1
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Best Local Similarity
Matches 115; Conserv
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APPLICANT: Danisco A/S
APPLICANT: Stbbesen, Ole
APPLICANT: Stbbesen, Ole
APPLICANT: Stbbesen, Ole
APPLICANT: Stbbesen, Ole
APPLICANT: Sovensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
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; TYPE: PRT
; ORGANISM: T.
US-11-170-653-33
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US-11-170-653-33
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SEQ ID NO 33
LENGTH: 190
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Best Local Similarity
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Publication No. US20050271769A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
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TYPE: PRT
ORGANISM: T.
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NUMBER OF SEQ ID NOS: 66
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APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
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                                       121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                                                                                                  61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
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QRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY
                                                                                                                                                                                       OTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGSFTVNWSNSGNFVAGKGWQPGTKNKVI
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                                                                                                                                                                                                                                                                               58.0%; Score 630.5; DB 7; 60.2%; Pred. No. 2.2e-51; ative 27; Mismatches 48;
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181 FSSGYARITVA 191

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CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: FOT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOPTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 223
TYPE: PRT
ORGANISM: T. reesei
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sozensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sen
FILE REFERENCE: 674509-2046
FULE REFERENCE: 674509-2046
FURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: GT/IB01/00426
PRIOR FILING DATE: 2001-03-08
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Best Local Similarity 59.2
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/11170653 Publication No. US20050271769A1
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CURRENT APPLICATION NUMBER: US/11/170,653
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
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59.2%;
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; Pred. No. 1.2e-50;
29; Mismatches 48;
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; ORGANISM: A. :
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NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 36
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Best Local Similarity
                                                                        215 QSSGSSSITV
                                                   181 FSSGYARITV 190
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                                                                                                                  96 TYSGTFTPSGNGYLSVYGWTTDPLIEYYIVESYGDYNPGSGGTYKGTVTSDGSVYDIYTA
                                                                                                                               37 RSTPSSTGENNGFYYSFWTDGGGDVTYTNGDAGAYTVEWSNVGNFVGGKGWNPG-SAQDI
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58.4%; Pred. No. 5.8e-50;
3n. Mismatches 47;
                               224
2006,
15:23:01
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Search completed: February 10, Job time: 9.72315 secs